

Copyright (c) 1993 - 2002 Compugen Ltd.	protein - protein search, using sw model									
on:	December 3, 2002, 14:35:53 ; Search time 35 Seconds (without alignments)									
title:	US-09-907-263-2									
refr. score:	941 1 DSYCPQGVYHPPONINSICCT.....CSNCIKSLECTKCLIPQIEN 161									
oring table:	BLOSUM62 Gapext 0.5									
searched:	908470 seqs, 133250620 residues Total number of hits satisfying chosen parameters: 908470									
minimum DB seq length:	0									
maximum DB seq length:	2000000000									
1st-processing:	Minimum Match 0% Maximum Match 100% Listing First 45 summaries									
database :	A_Geneseg_101002: 1: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1980.DAT: 2: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1981.DAT: 3: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1982.DAT: 4: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1983.DAT: 5: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1984.DAT: 6: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1985.DAT: 7: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1986.DAT: 8: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1987.DAT: 9: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1988.DAT: 10: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1989.DAT: 11: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1990.DAT: 12: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1991.DAT: 13: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1992.DAT: 14: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1993.DAT: 15: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1994.DAT: 16: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1995.DAT: 17: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1996.DAT: 18: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1997.DAT: 19: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1998.DAT: 20: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1999.DAT: 21: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA2000.DAT: 22: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA2001.DAT: 23: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA2002.DAT: *									
RESULTS	RESULT 1 ID AAR27496 ID AAR27496 standard; protein; 161 AA. XX AC XX DT 09-MAR-1993 (first entry) DE Native 30 kD TNF inhibitor. XX KW Tumour necrosis factor; ethylene glycol; pharmacokinetic; KW adult respiratory distress syndrome; rheumatoid arthritis; KW septic shock; pulmonary fibrosis; spacer. XX OS Homo sapiens. XX PN WO9216221-A. XX PD 01-OCT-1992. XX PF 13-MAR-1992; 92WO-US02122. XX PR 15-MAR-1991; 91US-0669862. PR 17-JAN-1992; 92US-0822296. PA (SYN) SYNERGEN INC. XX PI Arnes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC; XX DR WPI 1992-348933/42. XX PT New ethylene glycolated polypeptide(s) with improved pharmacokinetic properties - for treating a TNF and IL-1									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES									
sult	No.	Score	Match	Length	DB	ID	Description			
1	941	100.0	161	13	AAR27496		Native 30 kD TNF i			
2	941	100.0	161	19	AAW59664		Human soluble tumo			
3	941	100.0	161	19	AAW52267		Tumour necrosis in			
4	941	100.0	161	20	AAW8933		Human 30 kDa TNF i			
5	941	100.0	161	22	AAB37676		Tumour necrosis fa			
6	941	100.0	211	20	AAW89225		Tumour necrosis fa			
7	941	100.0	280	22	AAB66379		Tumour necrosis fa			
8	941	100.0	309	16	AAR70108		TNF-R-GBPH fusion			
9	941	100.0	311	20	AAW89229		Tumour necrosis fa			
10	941	100.0	336	18	AAW33360		TBP(20-190)/ICG-be			

PT mediated diseases e.g. adult respiratory distress syndrome,
 PT rheumatoid arthritis, septic shock etc.
 XX

PS Claim 54; Fig 2; 10pp; English.

XX The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmacokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. or native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495.

XX Sequence 161 AA;

Query	Match	Score	Length
Best Local Matches	Similarity 100 %;	Score 941;	DB 13;
Db 1	Pred. No. 0;	Score 941;	Length 161;
Db 1	Mismatches 0;	Score 941;	Length 161;
Db 1	Indels 0;	Score 941;	Length 161;
Db 1	Gaps 0;	Score 941;	Length 161;

CC Best Local Similarity 100 %; Pred. No. 2.4e-67; Mismatches 0; Indels 0; Gaps 0;

CC Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Query 1 DSVCPGQKYTHPPONNSICCTKCHGTYLYNDCPGPQDDTCRCESESFTASENHLRHC 60

CC Db 1 DSVCPGQKYTHPPONNSICCTKCHGTYLYNDCPGPQDDTCRCESESFTASENHLRHC 60

CC Query 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHWSLENFOCFNCSLCLNGTVHLSQE 120

CC Db 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHWSLENFOCFNCSLCLNGTVHLSQE 120

CC Query 121 KONTVCTCHAGFFLRENECVSCKSNSKSLCTKCLPQIEN 161

CC Db 121 KONTVCTCHAGFFLRENECVSCKSNSKSLCTKCLPQIEN 161

RESULT 2
AAW55664

ID AAW55664 standard; Protein; 161 AA.

AC AAW55664;

XX DT 28-SEP-1998 (first entry)

XX DE Human soluble tumour necrosis factor receptor type I.

XX KW Human; tumour necrosis factor; TNF; TNF receptor type I;

XX KW inflammatory disease; leukaemia; TNF binding protein;

XX KW anti-inflammatory drug; methotrexates.

OS Homo sapiens.

XX WO9824463-A2.

XX PD 11-JUN-1998.

XX PP 08-DEC-1997; 97WO-US22733.

XX PR 09-JUL-1997; 97US-005203.

XX PR 06-DEC-1996; 96US-003287.

XX PR 23-JAN-1997; 97US-0036355.

XX PR 07-FEB-1997; 97US-0039315.

XX PA (AMGE-) AMGEN INC.

XX PT Bendele AM, Edwards CK, Sennello RM;

XX WPI; 1998-333039/29.

XX DR N-PSDB; AAV41548.

PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -
 PT by administering tumour necrosis factor binding protein and at least
 PT one additional anti-inflammatory drug, e.g. methotrexate

PS Disclosure; Fig 1; 104pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.

XX Sequence 161 AA;

CC Best Local Similarity 100 %; Pred. No. 2.4e-67; Mismatches 0; Indels 0; Gaps 0;

CC Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Query 1 DSVCPGQKYTHPPONNSICCTKCHGTYLYNDCPGPQDDTCRCESESFTASENHLRHC 60

CC Db 1 DSVCPGQKYTHPPONNSICCTKCHGTYLYNDCPGPQDDTCRCESESFTASENHLRHC 60

CC Query 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHWSLENFOCFNCSLCLNGTVHLSQE 120

CC Db 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHWSLENFOCFNCSLCLNGTVHLSQE 120

CC Query 121 KONTVCTCHAGFFLRENECVSCKSNSKSLCTKCLPQIEN 161

CC Db 121 KONTVCTCHAGFFLRENECVSCKSNSKSLCTKCLPQIEN 161

RESULT 3
AAW52267

ID AAW52267 standard; Protein; 161 AA.

AC AAW52267;

XX DT 29-JUN-1998 (First entry)

XX DE Soluble tumour necrosis factor receptor.

XX KW Soluble tumour necrosis factor receptor; STNFTR; TNF-mediated disease;

XX KW tumour necrosis factor binding protein; autoimmune disease; arthritis;

XX KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;

XX KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNF.

OS Homo sapiens.

XX PN WO9801555-A2.

XX PD 15-JAN-1998.

XX PP 09-JUL-1997; 97WO-US12244.

XX PR 04-MAR-1997; 97US-0039192.

XX PR 09-JUL-1996; 96US-0021443.

XX PR 06-DEC-1996; 96US-003534.

XX PR 23-JAN-1997; 97US-0037337.

XX PR 07-FEB-1997; 97US-0039314.

XX PA (AMGE-) AMGEN INC.

XX PT Edwards CK, Fisher EF, Kieft GL;

XX DR WPI; 1998-101052/09.

XX DR N-PSDB; AAV41548.

PT Truncated and soluble forms of tumour necrosis factor receptor -
 PT useful for treating diseases involving factor, e.g. arthritis and
 PT adult respiratory distress syndrome

XX XX

PS Claim 1; Fig 1; 205pp; English.

XX XX

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This sequence is the human soluble tumour necrosis factor receptor (stTNFR). The protein was used to make the truncated stTNFR proteins of the inventors. The truncated stTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant stTNFR which may also be used for measuring the amount of stTNFR in samples and to raise antibodies against stTNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The stTNFR proteins are well suited to large scale production (since they lack the disadimination site in region 111-126, so are more stable *in vivo*; contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The product from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents the TNF inhibitor 30 kDa protein.

Sequence	161 AA;	AA SQ	Sequence	161 AA;
Query Match	100.0% ; Score 941; DB 19; Length 161;		Query Match	100.0% ; Score 941; DB 20; Length 161;
Best Local Similarity	100.0% ; Pred. No. 2.4e-67;		Best Local Similarity	100.0% ; Pred. No. 2.4e-67;
Matches 161; Conservative 0; Mismatches 0; Gaps 0;			Matches 161; Conservative 0; Mismatches 0; Gaps 0;	
' 1 DSVCPQKRYIHQNNSCCTRKHGTLYNCPGPQDTDRCRECGSFTASENHLRHCL 60		Qy 1 DSYCPQGKYIHPQNNSCCTRKHKGTYLYNDCPGPQDTDRCRECGSFTASENHLRHCL 60		
' 1 DSVCPQKRYIHQNNSCCTRKHGTLYNCPGPQDTDRCRECGSFTASENHLRHCL 60		Db 1 DSVCPQGKYIHPQNNSCCTRKHKGTYLYNDCPGPQDTDRCRECGSFTASENHLRHCL 60		
' 61 SCSKCRKEMGVQEISSCTVDRDTVCGRKNQYRHYSNENLFCFNCISCLNGTVHLSCQE 120		Qy 61 SCSKCRKEMGVQEISSCTVDRDTVCGRKNQYRHYSNENLFCFNCISCLNGTVHLSCQE 120		
' 61 SCSKCRKEMGVQEISSCTVDRDTVCGRKNQYRHYSNENLFCFNCISCLNGTVHLSCQE 120		Db 61 SCSKCRKEMGVQEISSCTVDRDTVCGRKNQYRHYSNENLFCFNCISCLNGTVHLSCQE 120		
' 121 KONTVCTCHAGFLRENECVCSNCNSCKSLECTKLCPQIEN 161		Qy 121 KONTVCTCHAGFLRENECVCSNCNSCKSLECTKLCPQIEN 161		
' 121 KONTVCTCHAGFLRENECVCSNCNSCKSLECTKLCPQIEN 161		Db 121 KONTVCTCHAGFLRENECVCSNCNSCKSLECTKLCPQIEN 161		

RESULT 4	
W89233	AAW89233 standard; Protein; 161 AA.
	AAW89233;
	04-MAR-1999 (first entry)
	Tumour necrosis inhibitor 30 kDa protein.
	Tumour necrosis factor receptor 1; TNFR 1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.
	Homo sapiens.
	WO9849305-A1.
RESULT 5	
W89233	AAB37676 standard; protein; 161 AA.
	XX
	AC AAB37676;
	XX
	DT 02-MAR-2001 (first entry)
	XX
	DE Human 30 kDa TNF inhibitor.
	XX
	KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; IL-1; inflammatory disease; degenerative disease; human.
	XX
	OS Homo sapiens.
	XX
	PN US6143866-A.
	XX

PR	01-NOV-2000;	95US-0375242.
PF	19-JAN-1995;	90US-055574
PR	19-JUL-1990;	93US-009366
PR	09-JUL-1993;	89US-038190
PR	18-JUL-1989;	89US-045329
PR	11-DBC-1989;	
PR	07-FEB-1990;	90US-0479661
XX		

(ANGE-1) AMGEN INC.
Squires C, King MW, Hale KK, Brewer MT, Thompson RC,
Vanderslice RW, Vannice J, Kohno T;
WPI; 2001-006443/01.
N-PSDB; AAC83945.

Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and autoimmune diseases induced by.

PT TNF -
 XX
 PS Claim 1; Fig 19; 82pp; English.

CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
 CC (see AAB3765 and AAB37685), which have TNF inhibitory activity. The
 novel TNF inhibitors of the present invention are useful as therapeutic
 agents for inhibiting the activity of TNF and interleukin (IL-1), and
 CC for treating inflammatory and degenerative diseases mediated by TNF. The
 CC 30 kDa TNF inhibitor can inhibit TNF alpha.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 22; Length 161;
 Best Local Similarity 100.0%; Pred. No. 2.4e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 QY 1 DSVCPQGKYIHPORNSICCTKCHKGTYLYNDCPGQDTPDCBESCSFTASBNHLRHC 60
 Db 1 DSVCPQGKYIHPORNSICCTKCHKGTYLYNDCPGQDTPDCBESCSFTASBNHLRHC 60
 QY 61 SCSKRKEMQVETTSCTVDRDITVGCGRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120
 Db 61 SCSKRKEMQVETTSCTVDRDITVGCGRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120
 QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161
 Db 121 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161

RESULT 6

ID AAWB9225
 XX
 AC AAWB9225;
 XX
 DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFBp 4.0.
 XX
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; inflammation; dimerisation domain; autoimmune disease; chimeric; fusion; apoptosis.
 KW Homo sapiens.
 OS Synthetic.
 PN WO9849305-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08631.
 PR 01-MAY-1997; 97US-0850188.
 XX
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S,
 XX
 DR WPI; 1999-03461/03.
 XX
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 XX
 PS Example 1; Fig 4; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 XX

CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFBp/OPG construct from
 CC the example of the present invention for creating TNFBp/OPG fusion
 CC proteins.

XX Sequence 211 AA;

Query Match 100.0%; Score 941; DB 20; Length 211;
 Best Local Similarity 100.0%; Pred. No. 3.1e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 QY 1 DSVCPQGKYIHPORNSICCTKCHKGTYLYNDCPGQDTPDCBESCSFTASBNHLRHC 60
 Db 41 DSVCPQGKYIHPORNSICCTKCHKGTYLYNDCPGQDTPDCBESCSFTASBNHLRHC 100
 QY 61 SCSKRKEMQVETTSCTVDRDITVGCGRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120
 Db 101 SCSKRKEMQVETTSCTVDRDITVGCGRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 160
 QY 121 KONTVCTCHAGFFLRENECVS-CSNCKSLECTKLCLPQIEN 161
 Db 161 KONTVCTCHAGFFLRENECVS-CSNCKSLECTKLCLPQIEN 201

RESULT 7

ID AAB65979
 ID AAB65979 standard; Protein; 280 AA.
 XX
 AC AAB65979;
 XX
 DT 19-APR-2001 (first entry)

DE Tnfrf protein.
 XX
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.
 KW Unidentified.
 XX
 PN WO200103719-A2.
 XX
 PR 18-JAN-2001.
 XX
 PR 07-JUL-2000; 2000WO-US18667.
 XX
 PR 09-JUL-1999; 99US-0359670.
 PR 09-DEC-1999; 99US-0457647.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 XX
 DR WPI; 2001-103031/11.
 XX
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of
 PT interleukin and tumor necrosis factor alpha -
 XX
 PS Disclosure; Fig 2; 316pp; English.

PI Boyle WJ, Wooden S;
XX
DR
WPI; 1999-034661/03.

XX
PT New chimeric osteoprotegerin polypeptides - contain the
osteoprotegerin dimerisation domain and a heterologous sequence,
useful to treat TNF and TNFR-mediated disorders

XX
PS Example 1; FIG 4; 92pp; English.

XX
CC The present invention describes a chimeric polypeptide (Al), comprising
an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
amino acid sequence. Also described are: (1) a multi-mer polypeptide
comprising covalently associated Al monomers; (2) an isolated nucleic
acid encoding (Al); (3) an expression vector comprising the nucleic acid
sequence, and (4) a host cell transformed or transfected with the
expression vector so that the nucleic acid is expressible. The products
from the present invention are useful to treat a variety of disorders
including those related to receptor binding. Compositions comprising
tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
are used to treat TNF and TNFR-mediated disorders such as inflammation,
autoimmune diseases and disorders related to excessive apoptosis. The
chimeras are also useful for detecting molecules which interact with
fused heterologous sequences to identify potential new receptors and
ligands. The present sequence represents a TNFbp/OPG construct from
the example of the present invention for creating TNFbp/OPG fusion
proteins.

XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 941; DB 20; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.4e-67; Indels 0; Gaps 0;

Matches 161; Conservative 0; Mismatches 0; Caps 0; Gaps 0;

QY 1 DSVVPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRRCESSFTASENHLRHCL 60

Db 41 DSVVPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRRCESSFTASENHLRHCL 100

QY 61 SCSKCRKEMQVKESSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSTLNGTVHLSQE 120

Db 101 SCSKCRKEMQVKESSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSTLNGTVHLSQE 160

QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161

Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 201

RESULT 10
AAW33360

ID AAW33360 standard; Protein; 336 AA.
XX
AC AAW33360;
XX
DT 19-MAR-1998 (first entry)

XX DE TBP(20-190)/hcg-beta fusion protein.
XX Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW beta subunit; hcg-beta.
XX Homo sapiens.
XX
OS Homo sapiens.
XX
PN WO9730161-A1.
XX
PD 21-AUG-1997.

XX
PP 20-FEB-1997; 97WO-US02315.
XX
PR 20-FEB-1996; 96US-0011936.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PT Campbell RK, Chappel SC, Jameson BA;

XX
DR
WPI; 1997-425036/39.
XX
DR
N-PSDB; AAT94022.

XX
PT Hybrid dimeric protein comprising two co-expressed units - each
based on receptor or ligand and a subunit of a heterodimeric
hormone, especially FSH, for inducing follicular maturation

XX
PS Example; Pages 39-40; 60p; English.

XX
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
acid sequences, each consisting of a homodimeric or heterodimeric
receptor chain or ligand, with ligand-receptor binding activity,
bound directly or via a peptide linker to a subunit of a heterodimer
heterodimeric protein hormone capable of forming a heterodimer with
the hormone's other subunits. The fusion protein, e.g. the
thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
(hCG-beta) fusion protein denoted by the present sequence,
significantly increases the biological activity of the hormone
component reducing the requirement for hormone itself and the
number of injections needed.

XX
SQ Sequence 336 AA;

Query Match 100.0%; Score 941; DB 18; Length 336;
Best Local Similarity 100.0%; Pred. No. 4.7e-67; Indels 0; Gaps 0;

Matches 161; Conservative 0; Mismatches 0; Caps 0; Gaps 0;

QY 1 DSVVPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRRCESSFTASENHLRHCL 60

Db 23 DSVVPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRRCESSFTASENHLRHCL 82

QY 61 SCSKCRKEMQVKESSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSTLNGTVHLSQE 120

Db 83 SCSKCRKEMQVKESSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSTLNGTVHLSQE 142

QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161

Db 143 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 183

RESULT 11
AAW89228

ID AAW89228 standard; Protein; 366 AA.
XX
AC AAW89228;
XX
DT 04-MAR-1999 (first entry)

XX DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.
XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO989305-A1.
XX
PD 05-NOV-1998.
XX
PP 29-APR-1998; 98WO-US08631.
XX
PR 01-MAY-1997; 97US-0850188.

XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
DR WPI; 1999-034661/03.
XX
PT New chimeric osteoprotegerin polypeptides - contain the

XX
PI Campbell RK, Chappel SC, Jameson BA;

PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 XX Example 1; Fig 4; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimeric polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 XX

SQ Sequence 366 AA;
 Query Match 100.0%; Score 941; DB 20; Length 366;
 Best Local Similarity 100.0%; Pred. No. 5.1e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGKYIHP QNNNSICCTPKCHKGTYLNDCPGGQDTDCRECEGSFTASENNHLRHCL 60
 Db 41 DSVCPQGKYIHP QNNNSICCTPKCHKGTYLNDCPGPQDTDCRECEGSFTASENNHLRHCL 100
 Qy 61 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENLFCQCNCSLCLNGTVHLSQE 120
 Db 101 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENLFCQCNCSLCLNGTVHLSQE 160
 Qy 121 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLQPQEN 161
 Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLQPQEN 201

RESULT 13

AAW89227
 ID AAW89227 standard; Protein; 397 AA.
 XX
 AC AAW89227;
 XX
 DT 04-MAR-1999 (first entry)

XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
 XX
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
 XX
 AC AAR07449;
 XX
 DT 29-JAN-1991 (first entry)
 XX
 DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
 XX
 KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
 KW pTNF-BP15; infectious disease; parasitic disease; cachexia;
 KW autoimmune disease; shock.
 XX
 OS Homo sapiens.
 XX
 PN EP393438-A.
 XX
 PD 24-OCT-1990.
 XX
 PF 06-APR-1990; 90EP-0106624.
 XX
 PR 21-JUN-1989; 89DE-3920282.
 XX
 PR 21-APR-1989; 89DE-3913101.
 PA (BOEHINGER INGELHEIMINT.
 XX
 PI Hauptmann R, Himmier A, Maurer-Fogy I, Stratowa C;
 XX
 DR WPI; 1990-321987/43.
 DR N-PSDB; AAQ06282.

XX DNA encoding TNF binding protein and TNF- receptor - used in
 PT tumour treatment and to understand mechanism to TNF action
 XX
 PS Disclosure: Fig 1(1-3); 51pp; German.
 XX
 CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of
 CC e.g. COS7 cells. The expressed proteins are useful
 CC prophylactically and therapeutically to control disorders which
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
 CC respiratory distress syndrome etc., or side effects of treatment with
 CC TNF-alpha). They can also be used as diagnostic reagents for
 CC assaying TNF and in study of TNF-receptor interactions
 CC See also AAQ06282-Q00285.
 XX
 SQ Sequence 371 AA;
 Query Match 100.0%; Score 941; DB 11; Length 371;
 Best Local Similarity 100.0%; Pred. No. 5.2e-67;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGKYIHP QNNNSICCTPKCHKGTYLNDCPGGQDTDCRECEGSFTASENNHLRHCL 60
 Db 41 DSVCPQGKYIHP QNNNSICCTPKCHKGTYLNDCPGPQDTDCRECEGSFTASENNHLRHCL 100
 Qy 61 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENLFCQCNCSLCLNGTVHLSQE 120
 Db 101 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENLFCQCNCSLCLNGTVHLSQE 160
 Qy 121 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLQPQEN 161
 Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLQPQEN 201

RESULT 14

AAW89227
 ID AAW89227 standard; Protein; 397 AA.
 XX
 AC AAW89227;
 XX
 DT 04-MAR-1999 (first entry)
 XX
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
 XX
 AC AAR07449;
 XX
 DT 29-JAN-1991 (first entry)
 XX
 DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
 XX
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9849305-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08631.
 XX
 PR 01-MAY-1997; 97US-0850188.
 XX
 PA (AMGEN INC.
 PA Boyle WJ, Wooden S;
 XX
 DR WPI; 1999-034661/03.
 XX
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimer domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 PT
 PS Example 1; Fig 4; 92pp; English.
 XX
 CC The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated Al monomers; (2) an isolated nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFbp/OPG construct from the example of the present invention for creating TNFbp/OPG fusion proteins.

XX
SQ Sequence 397 AA;

Query	Match	Score	DB	Length
QY 1	DSVCPOGKYTHPQQNSICCTKCHKGTYLYNDCPGPQDTCRCECSSFTASEHNHLCL	100.0%	20	397
Db 41	DSVCPOGKYTHPQQNSICCTKCHKGTYLYNDCPGPQDTCRCECSSFTASEHNHLCL	100.0%	20	397
Qy 61	SCSKRKEMQVEISCTVDRDTWGCRRNQYRHYSNLFOCFNCSLCLANGIVHUSCQE	120		
Db 101	SCSKRKEMQVEISCTVDRDTWGCRRNQYRHYSNLFOCFNCSLCLANGIVHUSCQE	160		
Qy 121	KONTVCTCHAGFFRENECVSCSNCKSSELECTKUCLPQIEN	161		
Db 161	KONTVCTCHAGFFRENECVSCSNCKSSELECTKUCLPQIEN	201		

RESULT 14

AAW89226 standard; Protein; 417 AA.

ID AAW89226;
XX AC AAW89226;

XX DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/196.

XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.

XX OS Homo sapiens.

OS Synthetic.

XX PN W09849305-A1.

XX PD 05-NOV-1998.

XX PP 98WO-US08631.

XX PR 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX PI Boyle WJ, Wooden S;

XX DR WPI; 1999-03461/03.

XX New chimeric osteoprotegerin polypeptides - contain the osteoprotgerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92PP; English.

XX
SQ Sequence 417 AA;

Query	Match	Score	DB	Length
QY 1	DSVCPOGKYTHPQQNSICCTKCHKGTYLYNDCPGPQDTCRCECSSFTASEHNHLCL	100.0%	20	417
Db 41	DSVCPOGKYTHPQQNSICCTKCHKGTYLYNDCPGPQDTCRCECSSFTASEHNHLCL	100.0%	20	417
Qy 61	SCSKRKEMQVEISCTVDRDTWGCRRNQYRHYSNLFOCFNCSLCLANGIVHUSCQE	120		
Db 101	SCSKRKEMQVEISCTVDRDTWGCRRNQYRHYSNLFOCFNCSLCLANGIVHUSCQE	160		
Qy 121	KONTVCTCHAGFFRENECVSCSNCKSSELECTKUCLPQIEN	161		
Db 161	KONTVCTCHAGFFRENECVSCSNCKSSELECTKUCLPQIEN	201		

RESULT 15

AAW89224 standard; Protein; 420 AA.

ID AAW89224;
XX AC AAW89224;

XX DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.

XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.

XX OS Homo sapiens.

OS Synthetic.

XX PN W09849305-A1.

XX PD 05-NOV-1998.

XX PP 98WO-US08631.

XX PR 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX PI Boyle WJ, Wooden S;

XX DR WPI; 1999-03461/03.

XX New chimeric osteoprotegerin polypeptides - contain the osteoprotgerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92PP; English.

XX
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transfected or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG Chimers
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 XX

Sequence 420 AA:

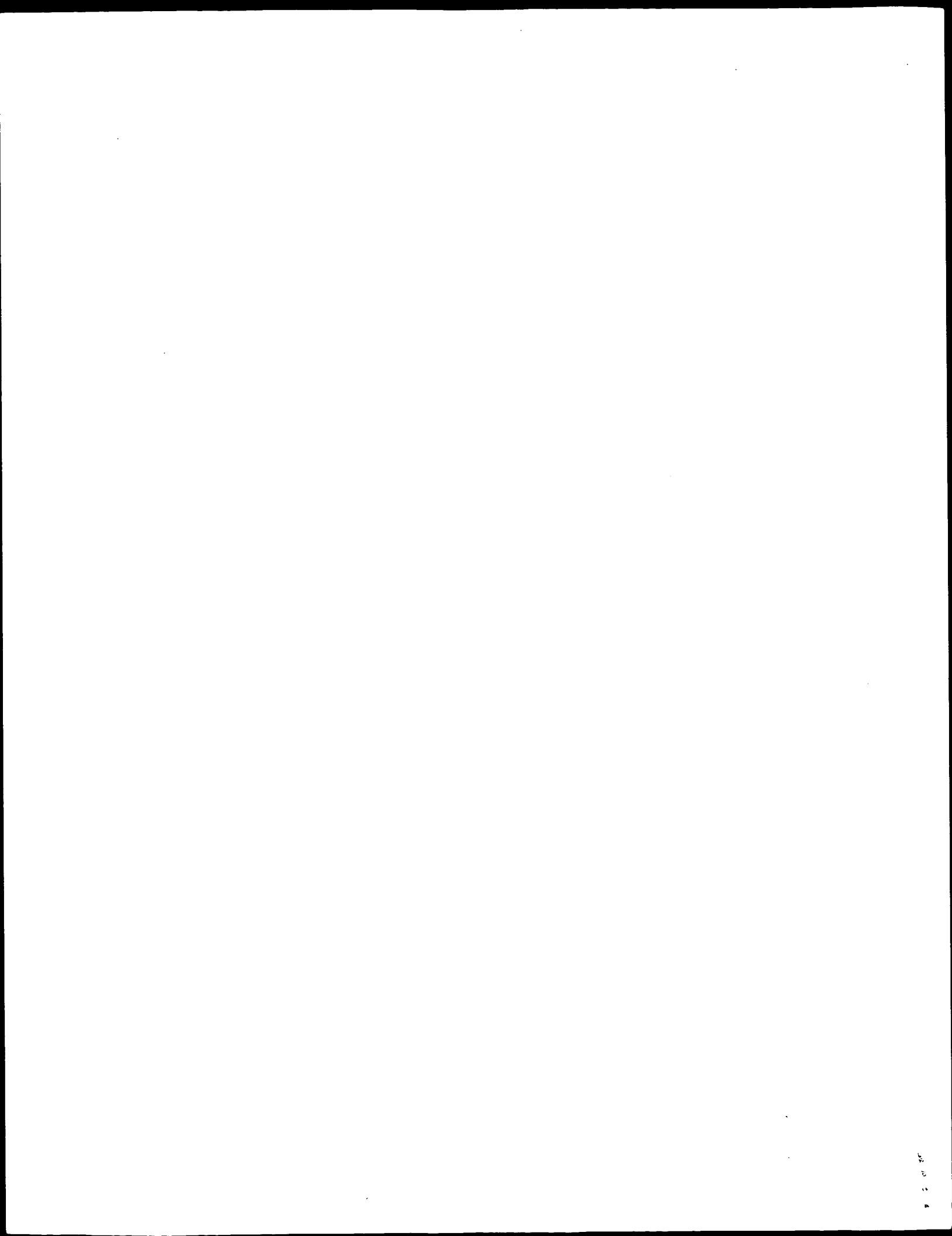
Score	941;	DB	20;	Length	420;
Query Match	100.0%;	Pred.	No.	5.	8e-67;
Best Local Similarity	100.0%;	Mismatches	0;	Indels	0;
Matches	161;	Conservative	0;	Gaps	0;

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Qy      1 DSVCPQGKYIHPQNNNSICCTKCHKGTYLNDCPGPQDQTDCRECESGSTASENHLRHCL 60
Db      41 DSVCPQGKYIHPQNNNSICCTPKCHKGTYLNDCPGPQDQTDCRECESGSTASENHLRHCL 100
Qy      61 SCSKCRKEMGQVEISSCTVDRDTVGCRKNQYRHYSENLFQOCNCNSLCLNGTVHLSQE 120
Db      101 SCSKCRKEMGQVEISSCTVDRDTVGCRKNQYRHYSENLFQOCNCNSLCLNGTVHLSQE 160
Qy      121 KONTVCTCHAGFLENECVCSNCKSLECTKLQLPQIEN 161
Db      161 KONTVCTCHAGFLENECVCSNCKSLECTKLQLPQIEN 201

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Search completed: December 3, 2002, 14:40:05
 Job time : 37 secs



GenCore version 5.1.3
 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2002, 14:39:28 ; Search time 15 seconds

(without alignments)
 315.806 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCPQSKYIHPQNNNCCCT.....CSNCCKSLECTKLQLPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/ptcdatal1/iaa/5A_COMB_pep:
 2: /cgn2_6/ptcdatal1/iaa/5B_COMB_pep:
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 4: /cgn2_6/ptcdatal1/iaa/6B_COMB_pep:
 5: /cgn2_6/ptcdatal1/iaa/PCUTUS_COMB_pep:
 6: /cgn2_6/ptcdatal1/iaa/backfiles1_pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	161	4	US-09-326-394-2
2	941	100.0	280	3	US-08-974-022-16
3	941	100.0	280	4	US-08-795-445A-46
4	941	100.0	280	4	US-08-795-447A-46
5	941	100.0	280	4	US-08-974-186-46
6	941	100.0	280	4	US-08-795-446B-46
7	941	100.0	280	4	US-08-706-945D-132
8	941	100.0	336	4	US-08-804-166-8
9	941	100.0	336	4	US-08-910-991-8
10	941	100.0	455	1	US-08-050-319B-25
11	941	100.0	455	1	US-08-321-668-2
12	941	100.0	455	1	US-08-837-941-2
13	941	100.0	455	2	US-08-126-016-2
14	941	100.0	455	2	US-08-465-982-25
15	941	100.0	455	4	US-08-815-1469-5
16	941	100.0	455	4	US-09-006-355A-3
17	941	100.0	455	4	US-09-527-235A-5
18	941	100.0	455	4	US-08-054-970-2
19	941	100.0	455	4	US-09-565-918-4
20	941	100.0	455	4	US-09-573-986-3
21	930.5	98.9	909	4	US-09-013-889A-4
22	930.5	98.9	909	4	US-09-448-886A-4
23	928	98.6	285	4	US-08-804-166-6
24	928	98.6	285	4	US-08-10-991-6
25	925.5	98.4	453	4	US-09-413A-5
26	924	98.2	199	1	US-08-050-319B-48
27	924	98.2	199	2	US-08-465-982-48

ALIGNMENTS

RESULT 1
 US-09-326-394-2
 ; Sequence 2, Application US/09326394
 ; Patent No. 6306820
 ; GENERAL INFORMATION:
 ; APPLICANT: Berdele, Alison M.
 ; APPLICANT: Senello, Regina M.
 ; APPLICANT: Edwards, Carl K.
 ; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING PROTEIN FOR TREATING TNF-MEDIATED DISEASES
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavenland Drive
 ; CITY: Thousand Oaks
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/326,394;
 ; FILING DATE: 08-DEC-1997
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/032,587
 ; FILING DATE: 06-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,355
 ; FILING DATE: 23-JAN-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/039,315
 ; FILING DATE: 07-FEB-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/052,023
 ; FILING DATE: 09-JUL-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zindrick, Thomas K.
 ; REGISTRATION NUMBER: 32,185
 ; REFERENCE/DOCKET NUMBER: A-430D
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 161 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-09-326-394-2

NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: One Amgen Center Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91362-1789

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,447A
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-378D2
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 SEQUENCE:
 DSCSKRKEMGQVEISSCTVDRDTCGGCRKKNQYRHWSNLFQCFNCSLCLNGTVHLSQE 60
 DSCSKRKEMGQVEISSCTVDRDTCGGCRKKNQYRHWSNLFQCFNCSLCLNGTVHLSQE 100
 DSCSKRKEMGQVEISSCTVDRDTCGGCRKKNQYRHWSNLFQCFNCSLCLNGTVHLSQE 120
 DSCSKRKEMGQVEISSCTVDRDTCGGCRKKNQYRHWSNLFQCFNCSLCLNGTVHLSQE 160
 DSCSKRKEMGQVEISSCTVDRDTCGGCRKKNQYRHWSNLFQCFNCSLCLNGTVHLSQE 180
 DSCSKRKEMGQVEISSCTVDRDTCGGCRKKNQYRHWSNLFQCFNCSLCLNGTVHLSQE 160

Query Match 100.0%; Score 941; DB 4; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.7e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-08-974-186-46
 Sequence 46, Application US/08974186
 Patent No. 6284440

GENERAL INFORMATION:
 APPLICANT: Boyle, William J.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Boyle, William J.
 APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi
 TITLE OF INVENTION: OSTEOPROTEGERIN
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1840 Dehavenland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,446B
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: A-378
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 CLASSIFICATION:
 US-08-795-446B-46

Query Match Similarity 100.0%; Score 941; DB 4; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.7e-76; Mismatches 0; Indels 0; Gaps 0;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLYNDCPGQDTPCRECGSFTASENHLRHCL 60
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLYNDCPGQDTPCRECGSFTASENHLRHCL 100

QY 61 SCSKCKRKEMGQVEISSCTVDRDTVGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSQE 120
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QY 121 KONTVCTCHAGFFLRENCEVSCSNCKSLECLKLQPIEN 161
 Db 161 KONTVCTCHAGFFLRENCEVSCSNCKSLECLKLQPIEN 201

RESULT 7

US-08-706-945D-132

; Sequence 132, Application US/08/0706945D

; Patent No. 6369027

; GENERAL INFORMATION:

; APPLICANT: Boyle, William

; APPLICANT: Lacey, David

; APPLICANT: Calzone, Frank

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: Osteoprotegerin

; FILE REFERENCE: A-378CIP

; CURRENT APPLICATION NUMBER: US/08/706, 945D

; CURRENT FILING DATE: 1996-09-03

; PRIOR APPLICATION NUMBER: 08/557, 788

; PRIOR FILING DATE: 1995-12-22

; NUMBER OF SEQ ID NOS: 145

; SEQ ID NO: 132

; LENGTH: 280

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-706-945D-132

Query Match Similarity 100.0%; Score 941; DB 4; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.7e-76; Mismatches 0; Indels 0; Gaps 0;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLYNDCPGQDTPCRECGSFTASENHLRHCL 60
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLYNDCPGQDTPCRECGSFTASENHLRHCL 100

QY 61 SCSKCKRKEMGQVEISSCTVDRDTVGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSQE 120
 Db 101 SCSKCKRKEMGQVEISSCTVDRDTVGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSQE 160

QY 121 KONTVCTCHAGFFLRENCEVSCSNCKSLECLKLQPIEN 161
 Db 161 KONTVCTCHAGFFLRENCEVSCSNCKSLECLKLQPIEN 201

RESULT 8

US-08-804-166-8

; Sequence 8, Application US/08804166

; Patent No. 6193972

; GENERAL INFORMATION:

; APPLICANT: Campbell, Robert K.

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Chappel, Scott C.

; TITLE OF INVENTION: HYBRID PROTEINS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street N.W., Ste. 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

US-08-804-166-8

; Sequence 8, Application US/08804166

; Patent No. 6193972

; GENERAL INFORMATION:

; APPLICANT: Campbell, Robert K.

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Chappel, Scott C.

; TITLE OF INVENTION: HYBRID PROTEINS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street N.W., Ste. 300
 CITY: Washington
 STATE: D.C.

RESULT 9

US-08-910-991-8

; Sequence 8, Application US/08910991

; Patent No. 6194177

; GENERAL INFORMATION:

; APPLICANT: Campbell, Robert K.

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Chappel, Scott C.

; TITLE OF INVENTION: HYBRID PROTEINS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street N.W., Ste. 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

Computer Readable Form:

Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patentent Release #1.0, Version #1.30

Application Number: US/08/910,991

Filing Date: 1996-09-03

Classification: 530

COUNTRY: USA
 ZIP: 22207
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/804, 166
 FILING DATE:
 CLASSIFICATION:
 NAME: Browdy, Roger L.
 REGISTRATION NUMBER: 25, 618
 REFERENCE DOCKET NUMBER: CAMPBELL=2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEX/FAX: (202) 737-3528
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 amino acid
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-804-166-8

Query Match Similarity 100.0%; Score 941; DB 4; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.2e-76; Mismatches 0; Indels 0; Gaps 0;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 23 DSVCPQGKYTHPONNSICCTKCHKGTYLYNDCPGQDTPCRECGSFTASENHLRHCL 82

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QY 121 KONTVCTCHAGFFLRENCEVSCSNCKSLECLKLQPIEN 161
 Db 143 KONTVCTCHAGFFLRENCEVSCSNCKSLECLKLQPIEN 183

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/804,166
 FILING DATE: 20 February 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/011,936
 FILING DATE: 20 February 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: YUN, Allen C.
 REGISTRATION NUMBER: 37,971
 REFERENCE/DOCKET NUMBER: CAMPBELL-2B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5197
 TELEFAX: (202) 737-3528
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-910-911-8

Query Match 100.0%; Score 941; DB 4; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.2e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10 - US-08-050-319B-25
 Sequence 25, Application US/08050319B
 Patent No. 5531345
 GENERAL INFORMATION:
 APPLICANT: M. Feldmann, P.W. Gray,
 TITLE OF INVENTION: Modified human TNF α (Tumor
 Title: Nerosis Factor alpha) Receptor
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Reed & Robbins
 STREET: 635 Bryant Street
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/050,319B
 FILING DATE: 10-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Robbins, Roberta L.
 REGISTRATION NUMBER: 33,208
 REFERENCE/DOCKET NUMBER: 5150-0030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 617-8999
 TELEFAX: (415) 327-3231
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:

Query Match 100.0%; Score 941; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-08-050-319B-25

Query Match 100.0%; Score 941; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-08-910-911-8

Query Match 100.0%; Score 941; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-08-050-319B-25

Query 1 DSYCPOGKYIHQNNSICCTKCHKGTYLYNDCPGQDTCRECESGSFTASENHLRHL 60
 Db 41 DSYCPOGKYIHQNNSICCTKCHKGTYLYNDCPGQDTCRECESGSFTASENHLRHL 100
 Qy 61 SCSKCRKEMGQVEISSCTVBDTVCCKRNQYRHWSNLQFCFNCSLCINGTVHLSQE 120
 Db 101 SCSKCRKEMGQVEISSCTVBDTVCCKRNQYRHWSNLQFCFNCSLCINGTVHLSQE 160
 Qy 121 KONTVCTCHAGFLRNECTVSNCNRKSLECTKLCLPQIEN 161
 Db 161 KONTVCTCHAGFLRNECTVSNCNRKSLECTKLCLPQIEN 201

Query Match 100.0%; Score 941; DB 4; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.2e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 11 - US-08-211-668-2
 Sequence 2, Application US/08321668
 Patent No. 5655559
 GENERAL INFORMATION:
 APPLICANT: WALLACH, David
 APPLICANT: BRAKEBUSCH, Cord
 APPLICANT: VAFOLOMEYEV, Eugene
 APPLICANT: BARKIN, Michael
 TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESS: BROWNY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/321,668
 FILING DATE: 12-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IL 107268
 FILING DATE: 12-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWNY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: WALLACH-13
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-08-910-911-8

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDCPGPQDTCRECESGFTASENHLRCL 60
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDCPGPQDTCRECESGFTASENHLRCL 100
 QY 61 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 120
 Db 101 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 160
 QY 121 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 161
 Db 161 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 201
 RESULT 12
 US-08-837-941-2
 Sequence 2, Application US/08837941
 Patent No. 5766917
 GENERAL INFORMATION:
 APPLICANT: WALLACH, David
 APPLICANT: BRAKEBUSCH, CORD
 APPLICANT: VARYOLOMEV, Eugene
 APPLICANT: BATKIN, Michael
 TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/837,941
 FILING DATE: 28-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/321,668
 FILING DATE: 12-OCT-1994
 APPLICATION NUMBER: IL 107268
 FILING DATE: 12-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BROMY, Roger L.
 NAME: BROMY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: WALLACH4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-837-941-2
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-126-016-2
 Query Match 100 %; Score 941; DB 1; Length 455;
 Best Local Similarity 100 %; Pred. No. 4,3e-76; Gaps 0;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDCPGPQDTCRECESGFTASENHLRCL 60
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDCPGPQDTCRECESGFTASENHLRCL 100
 QY 61 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 120
 Db 101 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 160
 QY 121 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 161
 Db 161 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 201

Db 101 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 160
 QY 121 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 161
 Db 161 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 201
 RESULT 13
 US-08-126-016-2
 Sequence 2, Application US/08126016
 Patent No. 581261
 GENERAL INFORMATION:
 APPLICANT: WALLACH, DAVID
 APPLICANT: NOPHAR, YARON
 APPLICANT: KEMPER, OLIVER
 APPLICANT: ENGELMANN, HARTMUT
 APPLICANT: BRAKEBUSCH, CORD
 APPLICANT: ADERA, DAN
 TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR (TBP-1)
 TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-1)
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/126,016
 FILING DATE: 24-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/625668
 FILING DATE: 13-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, ROGER L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: WALLACH4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-126-016-2
 Query Match 100 %; Score 941; DB 2; Length 455;
 Best Local Similarity 100 %; Pred. No. 4,3e-76; Gaps 0;
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 QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDCPGPQDTCRECESGFTASENHLRCL 60
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDCPGPQDTCRECESGFTASENHLRCL 100
 QY 61 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 120
 Db 101 SCSKCRKEMGQEISSTVDRDTVGCRKNQRYHWSNLFOCFNCSLCLNGTVHLSCQE 160
 QY 121 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 161
 Db 161 KONTVCTCHAGFIRENECVSCSNCKSLECKLCLPQEN 201

RESULT 14
 US-08-465-982-25
 Sequence 25, Application US/08465982
 Patent No. 5863786
 GENERAL INFORMATION:
 APPLICANT: M. Feldmann, P.W. Gray,
 TITLE OF INVENTION: Modified human TNFalpha (Tumor
 Necrosis Factor alpha) Receptor
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSED: Reed & Robbins
 STREET: 635 Bryant Street
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,982
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/050,319
 FILING DATE: 10-May-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Robbins, Roberta L.
 REGISTRATION NUMBER: 33,208
 REFERENCE/DOCKET NUMBER: 5150-0030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 347-3231
 TELEFAX: (415) 347-8999
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-465-982-25

Query Match 100.0%; Score 941; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

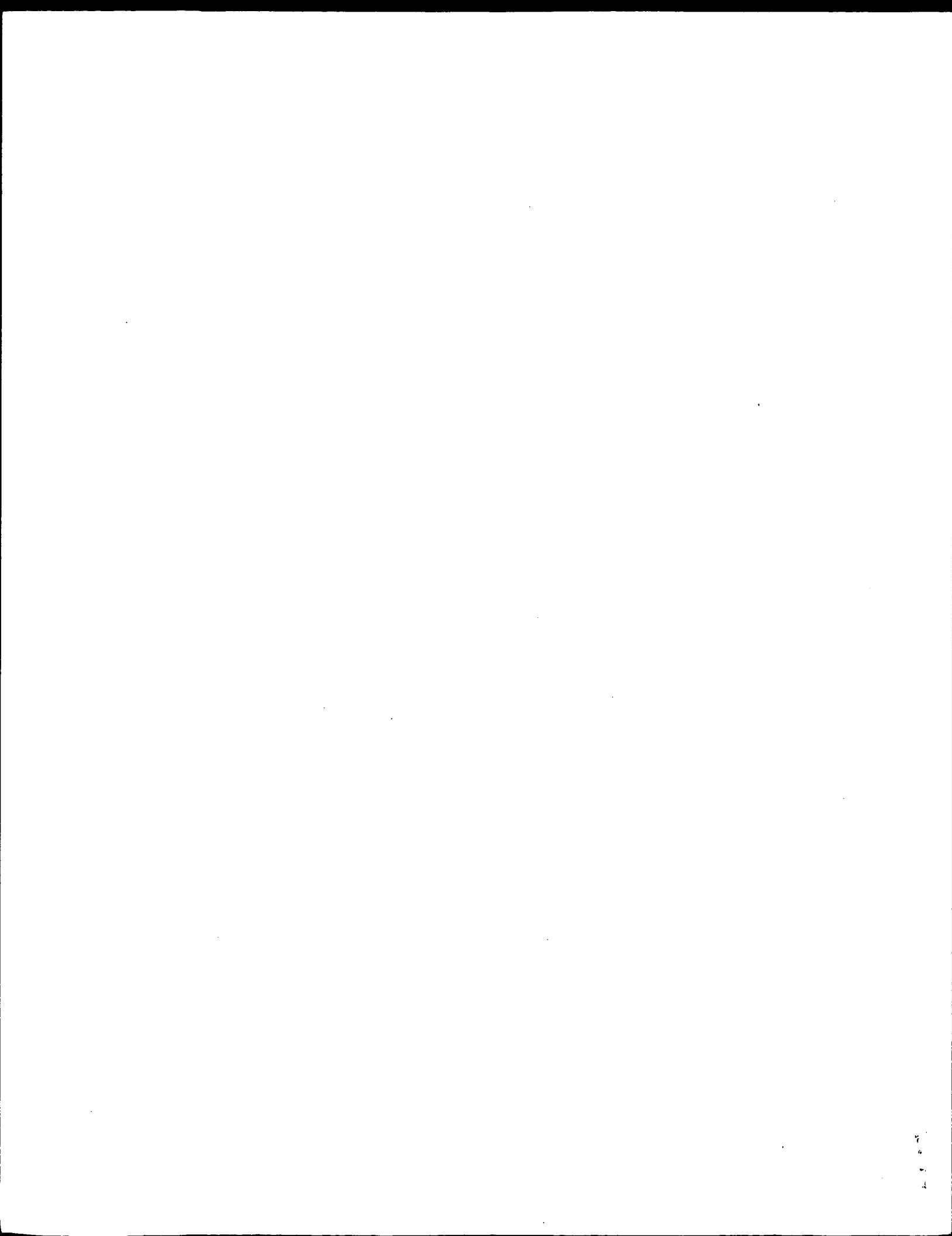
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 Db 101 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCNCISLCLNGTVHLSQE 160
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 Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 201

Query Match 100.0%; Score 941; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 60
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 Qy 61 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCNCISLCLNGTVHLSQE 120
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 Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 201

Search completed: December 3, 2002, 14:41:46
 Job time : 16 secs

RESULT 15
 US-08-815-469-5
 Sequence 5, Application US/08815169
 Patent No. 6153402
 GENERAL INFORMATION:
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Ni, Jian
 APPLICANT: Dixit, Vishva
 APPLICANT: Gentz, Reiner L.
 APPLICANT: Dillon, Patrick J.
 TITLE OF INVENTION: Death Domain Containing Receptors
 NUMBER OF SEQUENCES: 17



A;Cross-references: GB:M37764
 A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Lys, and TGA for residue 373 as Stop. The cDNA for the type I receptor was identical to the cDNA for the type II receptor.
 A;Reference number: S12057; MUID:91006021; PMID:1698610
 A;Accession: S12057
 A;Molecule type: mRNA
 A;Residues: 1-455 <NOP>
 A;Cross-references: EMBL:X55313; NID:937223; PIDN:CAA39021_1; PID:937224
 A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were expressed in *Saccharomyces cerevisiae*.
 R;Kemper, O.; Wallach, D.
 Gene 134: 209-216, 1993
 A;Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor receptor.
 A;Reference number: JT0758; MUID:94085779; PMID:8262379
 A;Accession: JT0758
 A;Molecule type: DNA
 A;Residues: 1-13 <KEM>
 R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 Eur. J. Immunol. 20: 1167-1174, 1990
 A;Title: Tumor necrosis factor inhibitor: purification, NH₂-terminal amino acid sequence, and biological activity.
 A;Reference number: A60231; MUID:90292116; PMID:2113477
 A;Accession: A60231
 A;Molecule type: protein
 A;Residues: X'55-53, 'X', 55-57 <SEC>
 R;Gattinger, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, B.W.B.; Le Proc. Natl. Acad. Sci. U.S.A. 87: 8781-8784, 1990
 A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor) from rat liver.
 A;Reference number: A382538; MUID:91062364; PMID:2174164
 A;Accession: A382538
 A;Molecule type: protein
 A;Residues: 41-60 <GAT>
 A;Experimental source: cancer patient serum
 R;Olsson, I.; Lantz, M.; Nilsson, B.; Petre, C.; Thyssell, H.; Grubb, A.; Adolf, G.
 Eur. J. Haematol. 42: 270-275, 1989
 A;Title: Isolation and characterization of a tumor necrosis factor binding protein from human urine.
 A;Reference number: A60594; MUID:89171156; PMID:2924890
 A;Accession: A60594
 A;Molecule type: protein
 A;Residues: 41-43, 'X', 45-53, 'V', 55-57, 'X', 60 <OLs>
 A;Experimental source: renal failure patient urine
 R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265: 1531-1536, 1990
 A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for a third.
 A;Reference number: A35010; MUID:90110215; PMID:2153136
 A;Accession: A35010
 A;Molecule type: protein
 A;Residues: 41-45 <BNG>
 A;Experimental source: normal urine
 R;Kojihara, J.; Asada, A.; Kirihara, S.; Kato, K.
 Biosci. Biotechnol. Biochem. 58: 2266-2268, 1994
 A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
 A;Reference number: JC2404; MUID:95128033; PMID:7765720
 A;Accession: JC2404
 A;Molecule type: protein
 A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
 A;Experimental source: urine
 C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (cachelin).
 C;Genetics:
 A;Gene: GDB:TNR1
 A;Cross-references: GDB:125913; OMIM:191190
 A;Map position: 12p13.2-12p13.2
 A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 255/3; 353/1
 C;Superfamily: tumor necrosis factor receptor type I; NGF receptor repeat homology
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
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 F;22-445/Domain: tumor necrosis factor receptor type I #status predicted <MAT>
 F;30-211/Domain: extracellular #status predicted <EXT>
 F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
 F;44-82/Domain: NGF receptor repeat homology <NGI>

F;84-126/Domain:	NGF receptor repeat homology	<NG3>
F;121-167/Domain:	NGF receptor repeat homology	<NG3>
F;168-196/Domain:	NGF receptor repeat homology	<NG4>
F;212-234/Domain:	transmembrane #status predicted	<MEM>
F;235-455/Domain:	intracellular #status predicted	<INT>
F;54,145,151/Binding site:	carbohydrate (Asn) (covalent)	#status predicted
Query Match	100 %;	Score 941; DB 1; Length 455;
Best Local Similarity	100.0 %;	Pred. No. 8.3e-62;
Matches	161;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	DSVCPOGKVYHQNNSICCTCKHGTYLYNDCPGGQGDTCRCESGSFFASENHIRHCL 60
QY	41	DSVCPOGKVYHQNNSICCTCKHGTYLYNDCPGGQGDTCRCESGSFFASENHIRHCL 100
Db	61	SCSKCRKEMGQEVSCTVTDRDVGCRKQYRHYSENIFQFCNCSLCINGTVHLSCQE 120
Db	101	SCSKCRKEMGQEVSCTVTDRDVGCRKQYRHYSENIFQFCNCSLCINGTVHLSCQE 160
QY	121	KONTVCTAGFLRNECVSNCNSCKSLECTKLQPQIN 161
Db	161	KONTVCTAGFLRNECVSNCNSCKSLECTKLQPQIN 201

tumor necrosis factor receptor pbs precursor - pig
 C:Species: Sus scrofa domesticus (domestic pig)
 C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
 C;Accession: JG4302; PC4093
 R;Suter, B.; Pauli, U.
 Gene 163, 263-266, 1995
 A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor
 A;Reference number: JG4302; MUID:96011645; PMID:7590278
 A;Accession: JG4302
 A;Molecule type: mRNA
 A;Residues: 1-61 <SUT>
 A;Cross-references: GB:U19994; NID:91141752; PIDN: AAC48499.1; PID:91141753
 A;Accession: PC4093
 A;Molecule type: protein
 A;Residues: 1-7 <SU2>
 A;Experimental source: kidney cell line 15
 C;Genetics:
 A;Gene: tnfR
 C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-461/Product: tumor necrosis factor receptor pbs 55 #status predicted <MAT>
 F:44-144/Domain: extracellular cysteine rich #status predicted <EXT>
 F:44-82/Domain: NGF receptor repeat homology <NGFR>
 F:84-267/Domain: NGF receptor repeat homology <NGFR>
 F:211-231/Domain: transmembrane #status predicted <TM>
 F:361-447/Domain: binding site carbohydrate (Asn) (covalent) #status predicted <SIT>
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 Matches 120; Conservative 12; Mismatches 22;

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Db      61 SSSCKRKEMQVEISCTVTBRTDVCGCRKQRYRHWSENIFQOCNSCLSLINGTHLSC 120
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      101 SCSCKRSSEMSDVEIISPCTVIRDTVGCRKQRYKWTSETLFOCLNSCLCPNGTVOLPC 160
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||
      121 KOMTVCVCHASFLRNBCVWSNCNCKSLATKLC 155
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      161 KQDTICNCHSGFLRDKECVSCVNCKNA-DCKNL 194
  
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GOMST1 tumor necrosis factor receptor 1 precursor - mouse
 C/N:Alternative names: tumor necrosis factor receptor, 55K
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence version 30-Jun-1992 #text change 01-Dec-2000
 C/Cross-references: A38634; B40254; S16677; S19021; 154532; 157826
 C/Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor 1A; Reference number: A38634; Reference number: A38634; Accession number: A38634; MUID:91187885; PMID:1849278
 A/Molecule type: mRNA
 A/Residues: 1-454 <LEW>
 A/Cross references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
 A/Reference number: R.G.; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Branman, C.I.; Copeland, N.G.; Jenkins, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.; Proc. Natl. Acad. Sci. U.S.A. 88, 2831-2834, 1991
 A/Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor 1A; Reference number: A40254; MUID:91246168; PMID:1645445
 A/Accession: B40254
 A/Molecule type: mRNA
 A/Residues: 1-454 <BAR>
 A/Cross references: EMBL:X59238; NID:953578; PIDN:CAA41922.1; PID:g53579
 A/Reference number: K.; Taylor-Pischick, D.A.; Cope, A.P.; Kissosergis, A.M.; Gray, P.W.; Feldmaier, J.; Immunol. 11, 3020-3026, 1991
 A/Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor 1A; Reference number: S16677; MUID:91285014; PMID:1647956
 A/Accession: S16677
 A/Molecule type: mRNA
 A/Residues: 1-454 <ROT>
 A/Cross references: EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:g54849
 A/Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line 1A; Reference number: 154532; MUID:94245292; PMID:8188324
 A/Accession: 154532
 A/Status: translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-454 <RES>
 A/Cross references: GB:L26349; PIDN:G430732; PIDN:AAA59361.1; PID:g430733
 A/Reference number: R.; Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
 A/Title: Genomic organization and promoter function of the murine tumor necrosis factor 1A; Reference number: 157826; MUID:93156721; PMID:8381516
 A/Accession: 157826
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-393; 'G' 395-454 <REB2>
 A/Cross references: GB: M76656; NID:9202100; PIDN:AAA40465.1; PID:g202102
 C/Comment: This protein is one of two distantly related receptors for both TNF-alpha (cα
 C/Genetics:
 A/Gene: TNFR-2
 C/Introns: 13/3 ; 65/1; 108/1; 184/2; 210/1; 248/1; 257/3 ; 353/1
 C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C/Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein
 C/Domain: signal sequence #status predicted <SIG>
 F/1-29/Domain: #status predicted <MAT>
 F/30-45/Domain: tumor necrosis factor receptor type 1 #status predicted <EXT>
 F/30-212/Domain: extracellular #status predicted <EXT>
 F/84-126/Domain: NGF receptor repeat homology <NG1>
 F/127-167/Domain: NGF receptor repeat homology <NG2>
 F/168-204/Domain: NGF receptor repeat homology <NG4>
 F/213-235/Domain: transmembrane #status predicted <MEM>
 F/236-454/Domain: intracellular #status predicted <INT>
 F/54, 151/202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	72.3%	Score 680;	DB 1;	Length 454;
Best Local Similarity	71.3%;	Pred. No.	9.1e-43;	
Matches 112;	Conservative	19;	Mismatches	26;
			Indels	0;
			Gaps	0;
Qy	1	DSVCPQGXKIHPPNNSICCTKCHKGTVLYNDPGPGDODTRECESGSFTASESNHLRHCL	60	
Db	41	DSVCPQGXKIHPPNNSICCTKCHKGTVLYNDPGPGDODTRECESGSFTASESNHLRHCL	60	
Qy	61	SCSKCRKMVGQEISSCTVDRDTVCGERKRNVQYRHNENLFCQFNGSLCNGTvhLUSQEB	120	
Db	101	SCSKCRKMVGQEISSCTVDRDTVCGERKRNVQYRHNENLFCQFNGSLCNGTvhLUSQEB	120	
Qy	121	KQNTVCTCHAGFFLRENECVCSNCCKSLECLKLCLP	157	
Db	161	TQNTVCNCHAGFFLRENECVCSHCKNNECMKLCLP	197	
RESULT 4				
GQRITI				
tumor necrosis factor receptor 1 precursor - rat				
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)				
C;Species: Rattus norvegicus (Norway rat)				
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999				
C;Accession: B36555;A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lar				
R;Hammer, A.; DNA Cell Biol. 9, 705-715, 1990				
A;Title: Molecular cloning and expression of human and rat tumor necrosis facto				
A;Reference number: A36555; MUID:91090841; PMID:1702293				
A;Accession: B36555;				
A;Molecule Type: mRNA				
A;Residues: 1-461 <HIM>				
A;Cross-references: CB;M63122; NID:9207361; PID:AAA42256.1; PID:9207362				
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachee				
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homolo				
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein				
F;1-29/Domain: signal sequence #status predicted <SIG>				
F;10-461/Domain: tumor necrosis factor receptor type 1 #status predicted <MAT>				
F;30-211/Domain: extracellular #status predicted <EXT>				
F;4-82/Domain: tumor necrosis factor binding protein #status predicted <TPB>				
F;84-126/Domain: NGF receptor repeat homology <NG2>				
F;127-167/Domain: NGF receptor repeat homology <NG3>				
F;168-204/Domain: NGF receptor repeat homology <NG4>				
F;212-334/Domain: transmembrane #status predicted <MEM>				
F;235-461/Domain: intracellular #status predicted <INT>				
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				
18;				
Mismatches				
33;				
Indels				
0;				
Gaps				
0;				
Query Match				
Best Local Similarity				
Matches 110;				
Conservative				

P:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 19.2%; Score 181; DB 2; Length 474;

Best Local Similarity 31.7%; Pred. No. 2.3e-06;

Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;

T2 protein - myxoma virus (strain Lausanne)

C;Species: myxoma virus

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999

C;Accession: A40566

R;Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.

A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor

A;Reference number: A40566; MUID:91335768; PMID:1651597

A;Molecule type: DNA

A;Residues: 1-126 <DPT>

A;Cross-references: GB:M95181; GB:M37976; PIDN:AA46632.1; PID:9332310

C;Keywords: glycoprotein

F;106-147/Domain: NGF receptor repeat homology <NG3>

F;166-181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 179.5; DB 1; Length 326;

Best Local Similarity 27.4%; Pred. No. 2.3e-06;

Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7;

T2 protein - myxoma virus T2 protein; NGF receptor repeat homology

C;Species: myxoma virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: B43692

R;Upton, C.; DeLange, A.M.; McFadden, G.

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <UPT>

A;Cross-references: GB:M17413

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology <NG2>

F;61-105/Domain: NGF receptor repeat homology <NG3>

F;106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 18.9%; Score 178; DB 2; Length 325;

Best Local Similarity 29.6%; Pred. No. 3e-06;

Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

Db 40 CQGKVIHPQNSICCTKCHKCTLYNDCPGPQDTCRECESGSFTASENHLRHCLSC- 62

Db 40 CQISQEYVYDRQAMCCKACPKPQQYKHFC-NKTSDFVCADEASMYTQWNPFTCLSCS 98

Qy 63 SKCRKEMQVEISSCTVDRDTYCGRKKNQY--RHYSWENLIFQCFNCSLCLING-TVHLS 117

Db 99 SCTTD-D-QVERTRACTKQQNVRVACEAGRCALKTH-SSCSRQCMRLSKGPFGVASS 154

Qy 118 COEKONTVC-TCHAGGFLRENECVS-CSNCRKSLCTKLCLP 157

Db 155 RAPNGNVYLCKRACAPGTF--SDTTSSTDVCRPHRICSIILAIP 193

RESULT 8

GO:00291

T2 protein - myxoma virus (strain Lausanne)

C;Species: myxoma virus

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 10-Sep-1999

C;Accession: A26431

R;Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.

A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor

A;Reference number: A40566; MUID:91335768; PMID:1651597

A;Molecule type: DNA

A;Residues: 1-126 <DPT>

A;Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756

A;Accession: A26431

R;Metzis, M.; Timmusk, T.; Alrikmees, R.; Sarma, M.; Herzenberg, L.A.; Shooter, E.M.

A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A;Reference number: A26431; MUID:87115899; PMID:307580

A;Accession: PH1229

A;Molecule type: mRNA

A;Residues: 1-425 <RAD>

A;Cross-references: GB:X051269

A;Accession: PH1229

R;Metzis, M.; Timmusk, T.; Alrikmees, R.; Sarma, M.; Herzenberg, L.A.; Shooter, E.M.

A;Title: Regulatory elements and transcriptional regulation by the rat nerve growth factor receptor.

A;Reference number: PH1229; MUID:9307038; PMID:146821

A;Accession: PH1229

A;Molecule type: DNA

A;Residues: 1-20 <MET>

A;Cross-references: GB:X11269

A;Accession: PH1229

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t

C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cell

C;Comment: The cysteine-rich region of the extracellular domain may form part or all of the extracellular domain, extracellular status predicted <EXT>

C;Genetics: A;Introns: 20/3

F;68-109/Domain: NGF receptor repeat homology <NG2>

F;110-148/Domain: NGF receptor repeat homology <NG3>

F;150-190/Domain: NGF receptor repeat homology <NG4>

F;198-249/Region: serine/threonine-rich

F;252-273/Domain: transmembrane #status predicted <MEM>

F;274-425/Domain: intracellular #status predicted <INT>

F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 9

B43692

T2 protein - rabbit fibroma virus

C;Species: rabbit fibroma virus, Shope fibroma virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: B43692

R;Upton, C.; DeLange, A.M.; McFadden, G.

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <UPT>

A;Cross-references: GB:M17413

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology <NG2>

F;61-105/Domain: NGF receptor repeat homology <NG3>

F;106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 18.9%; Score 178; DB 2; Length 325;

Best Local Similarity 29.6%; Pred. No. 3e-06;

Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

Db 34 EKDGCLCASCHPFGYASRLC-GPGSNVTCSPEDGFTASTNHA PACVSRGPCTGHLS- 91

Qy 13 QNNSTICCTKCHKGTYLYNDCPGPQDTCRECESGSFTASENHLRHCLSC- 71

Db 34 EKDGCLCASCHPFGYASRLC-GPGSNVTCSPEDGFTASTNHA PACVSRGPCTGHLS- 91

Qy 72 VEISSCTVDRDTYCGRKKNQY- 92

Db 92 -ESQCDKWRDRVCDCSAGNYCLLRQEQECRICA PAKTKCPAGYGVSGHTRTGVLC LTKCP 150

Qy 93 RHYNSENLFOCFNCSLCLING-TVHLSQEKONTVCTCHAGFFIRENEVCSNCRKSLEC 151

Db 151 RYTSDAVSSTETCTSSFPYISVFNLYPVNDSCITTAG---PNEVVKTSEFSVTLNH 206

Qy 152 TKLCLP 157

Db 207 TD-CDP 211

Query Match 18.8%; Score 176.5; DB 1; Length 425;

Best Local Similarity 30.9%; Pred. No. 4.6e-06;

Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

Db 33 CSTGLYTH--SGECKACKNLGBEVQAQP-GANQ-TVCEPLUDNVTSATEPCPKPC 87

Qy 63 SKRKEMGQVEITS-CIVDRDTVCGRKNOVRHYSNLFQCFNSLCLNGT-VHLSCORE 120
 C:Species: Mus musculus (house mouse)
 C;Superfamily: variola minor virus
 C;Keywords: alternative splicing; transmembrane protein
 C;Domain: NGF receptor repeat homology <NGF>

Qy 121 KONTVCT-TCAGFFFLPE---NECVSCSNCKSLECTKLCLP 157
 Db 142 KONTVCEBECPEGTYSDDEAHVDPCLPCIVCDTEROLRECTP 183

RESULT 11

gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C;Accession: I48854

R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994

A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A;Reference number: I48854; MUID:95178848; PMID:767384

A;Accession: I48854

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: I-459 <RES>

A;Cross-references: EMBL:X16401; PIDN:CA5981.1; PID:943831

C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology <NGF>

C;Domain: NGF receptor repeat homology <NGF>

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Matches 46; Conservative 23; Mismatches 72; Indels 13; Gaps 7;

Db 4 CPQGKYIHPQNNNCTKCHKGTYLYNDCPGPQDPTCRECESGSFRASENHRLRHCLSC- 62

Db 25 CQISQEYDVKRAQMCAKPPGQSYKHFQ-NKTSDFTVCADCEASMYTQVNQNPRTCLSCS 83

Qy 63 SKRKEMGQVEITS-CIVDRDTVCGRKNOVRHYSNLFQCFNSLCLNGT-VHLSCORE 117

Db 84 SSCSTD-QVETRACTKQNRVACEAGRCYALKTH-SGSQRQCMRLSKCGPGFVASS 139

Qy 118 CQEKKONTVCT-TCAGFFFLPE---NECVSCSNCKSLECTKLCLP 157

Db 140 RAPNGNVILCKRACAPGT--SDTFSSTDVCRPARICSILAI P 178

RESULT 12

B cell-associated surface molecule CD40, long splice form - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C;Accession: A446475; A66515

R;Torres, R.M.; Clark, B.A.

J; Immunol. 158, 620-626, 1992

A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A;Reference number: A46476; MUID:92105763; PMID:1370315

A;Accession: A446476

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: I-305 <TOR>

A;Cross-references: GB:M83312; NID:91553058

A;Note: this translation is not annotated in GenBank entry MUSCD40a, release 113.0

R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,

J; Immunol. 149, 3921-3926, 1992

A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A;Reference number: A46515; MUID:93094586; PMID:1281194

A;Accession: A46515

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: I-287, 'LV' <GR>

A;Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; N

A;Experimental source: BALB/c, liver

A;Note: sequence extracted from NCBI backbone (NCBIP:120357)

C;Comment: For an alternative splice form, see PIR:A46476.

C;Superfamily: C27 antigen; NGF receptor repeat homology

C;Keywords: alternative splicing; transmembrane protein

C;Domain: NGF receptor repeat homology <NGF>

C;Comment: For an alternative splice form, see PIR:A46476.
 C;Superfamily: C27 antigen; NGF receptor repeat homology
 C;Keywords: alternative splicing; transmembrane protein
 C;Domain: NGF receptor repeat homology <NGF>

Query Match 17.8%; Score 167.5; DB 2; Length 305; Best Local Similarity 29.8%; Pred. No. 1.7e-05; Matches 46; Conservative 23; Mismatches 72; Indels 13; Gaps 7;

Db 26 CSQKYLH--DQCCDLQPOSRLTSHCIAL-EKQCHCDSGEFSAQNNRECHQR 81

Db 64 KCRKEMGQVEITSCTVDRDTVCGRKNOVRHYSNLFQCFNSLCLNGT-VHLSCORE 63

Db 82 HCPNQGLRUVKKEGTAESDVTVCCKEQ--HCTSKOCEACQHTCIPGFGVMEMATT 139

Qy 123 NTIVC-TCHAGFFELR---NECVSCSNCKSLECTKLCLP 150

Db 140 DTVCHPCCPVGFSSNOSLFLERKCYPWTSCEDKNLE 173

RESULT 13

D72175 G2R protein - variola minor virus (strain Garcia-1966)

C;Species: variola minor virus

C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000

C;Accession: D72175

R;Sicheleikunov, S.N.; Totmenin, A.V.; Gutovov, V.V.; Safronov, P.F.; Massung, R.F.; Iopai, submitted to GenBank, March 1998

A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A;Accession: A72150

A;Status: preliminary

A;Molecule type: DNA

A;Residues: I-349 <SHC>

A;Cross-references: GB:Y16780; NID:95830555; PIDN:CB854798.1; PID:95830759

A;Experimental source: strain Garcia-1966

A;Gene: G2R

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.7%; Score 166.5; DB 2; Length 349; Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Conservative 19; Mismatches 64; Indels 43; Gaps 9;

Matches 46; Conservative 19; Mismatches 64; Indels 43; Gaps 9;

Db 4 CPQGKYIHPQNNNCTKCHKGTYLYNDCPGPQDPTCRECESGSFRASENHRLRHCLSC- 63

Db 32 CKDTFV--KRNHCCLSLPPGTYASRICKDSK-TNTQCTPCSGFTTSRNHLPAULCN 87

Qy 64 -KCRKEMGQVEITSCTVDRDTVCGRKNOVRHYSNLFQCF---NCSLCLNGT-VHLSCORE 117

Db 88 GRCSNS--NOVETSNTNHRICECSPGYY-----CLIKGSSGCKACVSQT---- 131

Qy 118 CQEKKONTVCT-TCAGFFFLPE---NECVSCSNCKSLECTKLCLP 161

Db 132 -----KCGIGGVSGHTSVGDVICSPCGFRTSYTSSTDKCEPVPN 174

RESULT 14

T28623 hypothetical protein G2R - variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000

C;Accession: T28623

Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus

A;Reference number: 220488; MUID:94088747; PMID:8264798

A;Accession: T28623

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-348 <MAS>

A:Cross-references: EMBL:L22579; PID:AAA60933_1; PID:g439102
 A:Experimental source: strain Bangladesh 1975
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 164; DB 2; Length 348;
 Best Local Similarity 27.8%; Pred. No. 3.3e-05;
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

Qy 4 CPQGKYTHPQQNSICCTKCHKGTYLYNDCPGQDDCREEGSFTASSNNHLRHCLSCS 63
 Db 31 CRDTEY--KRHNLCCLSCSPDTYASRLCDSK-TNTQCTCGSGFTSRNNHLPACLSCN 86
 Qy 64 -KCRKENGQVEISSCTVDRDTVGCRKNOVRHYWSENLFQCF----NCSLCLNGTVHLS 117
 Db 87 GRCNS--NQVETRSCTNTHNRCECSPGYY-----CLWKSSGGCKACVST--- 130
 Qy 118 COEKQNTVCTCHAGFFIRENECVS--CSNC 145
 Db 131 -----KCIGYGVSIGHTSGVDVTCSPC 152

RESULT 15

D36858
 Gene G4R protein - variola virus
 N;Alternate names: B28R protein (COP)
 C:Species: variola virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
 C:Accession: D36858; S46888; S32385; S35987
 R:Blinov, V.M.
 submitted to GenBank, November 1992
 A:Reference number: A36859
 A:Accession: D36858
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <BLI>
 A:Cross-references: GB:X69198; PID:9456758; PID:CAA49137_1; PID:9457087

A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R:Kolychukov, S.N.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, V.V.; Sandatkhiev, L.S.
 Submitted to the EMBL Data Library, April 1992
 A:Description: Nucleotide sequence analysis of the region of variola virus XHOI F O H P
 A:Reference number: S46868
 A:Accession: S46888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <KOL>
 A:Cross-references: EMBL:X67117; PID:9516428; PID:CAA37540_1; PID:9516449

A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R:Shchelkunov, S.N.; Blinov, V.M.; Sandatkhiev, L.S.
 FEBS Lett. 319, 80-83, 1993
 A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
 A:Reference number: S32385; MUID:93402284; PMID:8384129
 A:Accession: S32385
 A:Molecule type: DNA
 A:Residues: 31-168 <SHC>
 A:Cross-references: EMBL:X669198
 A:Experimental source: strain India-1967, ssp. major
 C:Genetics:

A:Gene: G4R
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology <NGF>

F:168-109/Domain: NGF receptor repeat homology <NG2>
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 17.4%; Score 164; DB 2;
 Best Local Similarity 27.8%; Pred. No. 3.3e-05;
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

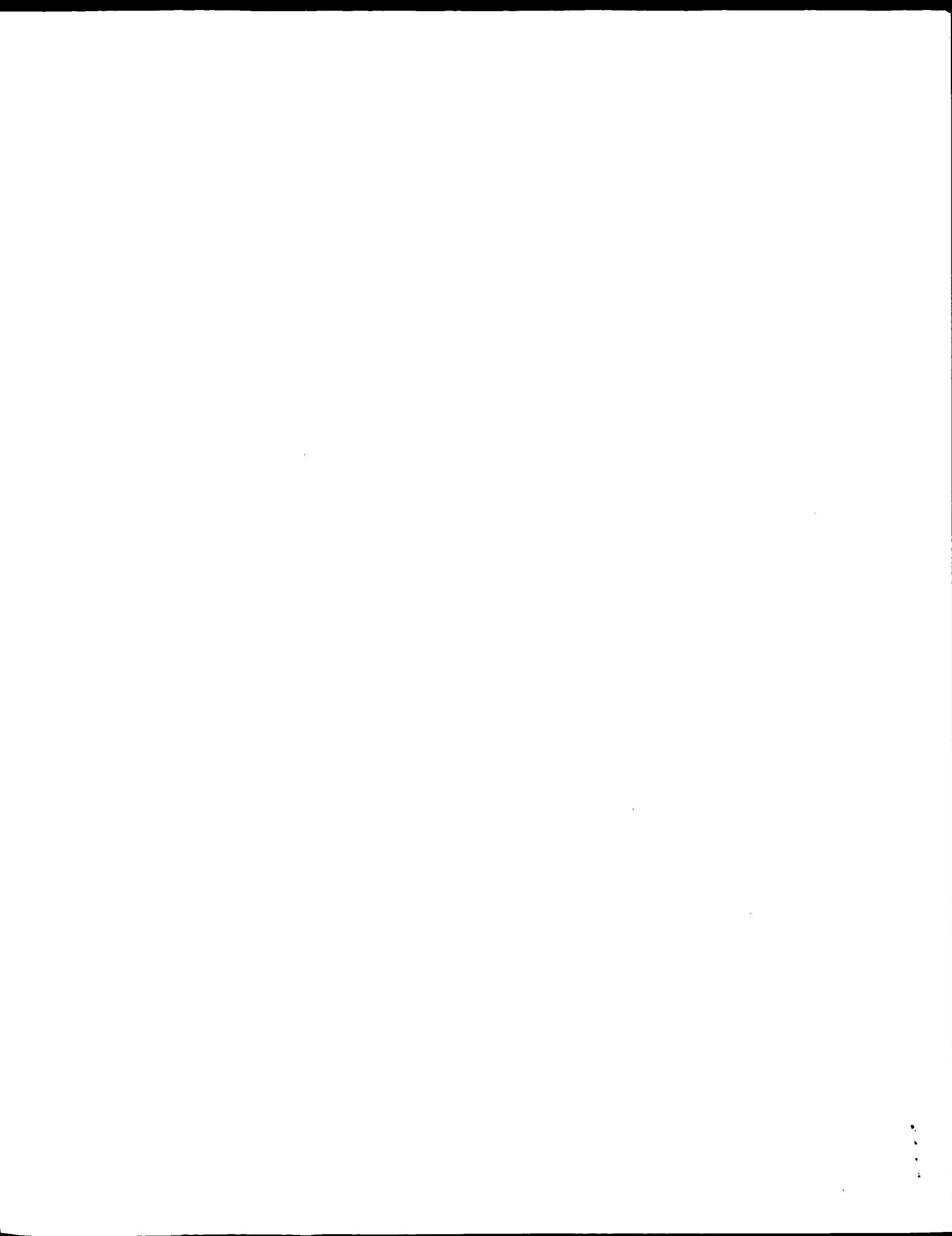
Qy 4 CPQGKYTHPQQNSICCTKCHKGTYLYNDCPGQDDCREEGSFTASSNNHLRHCLSCS 63
 Db 32 CRDTEY--KRHNLCCLSCSPDTYASRLCDSK-TNTQCTCGSGFTSRNNHLPACLSCN 87
 Qy 64 -KCRKENGQVEISSCTVDRDTVGCRKNOVRHYWSENLFQCF----NCSLCLNGTVHLS 117

A:Cross-references: EMBL:L22579; PID:AAA60933_1; PID:g439102
 A:Experimental source: strain Bangladesh 1975
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 164; DB 2; Length 348;
 Best Local Similarity 27.8%; Pred. No. 3.3e-05;
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

Qy 4 COEKQNTVCTCHAGFFIRENECVS--CSNC 145
 Db 132 -----KCIGYGVSIGHTSGVDVTCSPC 153

Search completed: December 3, 2002, 14:41:25
 Job time : 19 secs



Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	455	1 TRIA_HUMAN	P19438 homo sapien
2	716.5	76.1	461	1 TRIA_TIG	P5055 sus scrofa
3	680	72.3	454	1 TRIA_MOUSE	P25118 mus musculus
4	674.5	71.7	471	1 TRIA_BOVIN	O19131 bos taurus
5	669	71.1	461	1 TRIA_CAT	P23934 rattus norvegicus
6	200.5	21.3	176	1 TR23_MOUSE	Q93038 mus musculus
7	200.5	21.3	417	1 TR12_HUMAN	Q93038 h tumor necrosis factor receptor type I
8	198.5	21.1	180	1 TR22_MOUSE	Q9ee62 mus musculus
9	19.9	435	1	1 TNR3_HUMAN	P36941 homo sapien
10	182.5	19.4	427	1 TR16_HUMAN	P08138 homo sapien
11	181.5	19.3	417	1 TR16_MOUSE	Q920w1 mus musculus
12	181	19.2	474	1 TR1B_MOUSE	P25119 mus musculus
13	179.5	19.1	326	1 VT2_MYXVL	P29825 myxoma virus
14	178	18.9	325	1 VT2_SFVKV	P25943 shope fibroblast virus
15	176	18.8	332	1 TNR6_PIG	O77736 sus scrofa
16	176.5	18.8	425	1 TR16 RAT	P07174 rattus norvegicus
17	167.5	17.8	289	1 TNR5_MOUSE	P27512 mus musculus
18	167.5	17.8	415	1 TNR3_MOUSE	P26284 mus musculus
19	167	17.7	269	1 TNR5_BOVIN	P28203 bos taurus
20	166.5	17.7	323	1 TNR6_BOVIN	P51867 bos taurus
21	166.5	17.7	349	1 CRMB_CAMPY	Q8uyA7 cameipox virus
22	164	17.4	349	1 CRMB_VARV	P34015 variova virus
23	164	17.4	351	1 CRMB_COMPLEX	O73559 cowpox virus
24	164	17.4	401	1 T11B_HUMAN	P00300 homo sapiens
25	162.5	17.3	327	1 TNR6_MOUSE	P25446 mus musculus
26	161	17.1	461	1 TR1B_HUMAN	P20333 homo sapiens
27	154	16.8	401	1 T11B RAT	O88727 rattus norvegicus
28	154	16.4	401	1 T11B MOUSE	O08712 mus musculus
29	147	15.6	324	1 TNR6_RAT	Q63199 rattus norvegicus
30	145	15.4	416	1 TR16_CHICK	P18519 gallus gallus
31	142	15.1	283	1 TR14_HUMAN	Q32956 homo sapiens
32	142	15.1	386	1 T10D_HUMAN	Q3ubn6 homo sapiens
33	141	15.0	1680	1 FUR2_DRONE	P30432 drosophila

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40_*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

RESULT 1					
TRIA_HUMAN	ID	TRIA_HUMAN	STANDARD;	PRT;	455 AA.
AC P19438;	DT 01-FEB-1991 (Rel. 17, Created)	RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Granger G.A., Lentz R., Raab H., Kohn W.J., Goeddel D.V., Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tabuchi H., Lesslauer W., [2]	RP TISSUE=Placenta; PubMed=2158863; MEDLINE=90235288; Pubmed=2158863; SEQUENCE FROM N.A. [2]		
	DT 01-FEB-1991 (Rel. 17, Last sequence update)	RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human); Mammalia; Primates; Catarrhini; Hominidae; Homo. NCBI_Taxid=9606; RN [1]_TAXID=9606;	RP "Molecular cloning and expression of a receptor for human tumor necrosis factor 1 (TNF-R1) (P55) (CD120a) [Contains: Tumor necrosis factor receptor type I (TNFPI)]." [3]		
	DT 15-JUN-2002 (Rel. 41, Last annotation update)	RA Homo sapiens	RP SEQUENCE FROM N.A. [4]		
	DE Tumor necrosis factor receptor superfamily member 1A precursor (p60) (TNF-R1) (P55) (CD120a)	RA "Molecular cloning and expression of a receptor for human tumor necrosis factor 1 (TNF-R1) (P55) (CD120a)."	RP TISSUE=Placenta; PubMed=9015284; Pubmed=9015284; SEQUENCE FROM N.A. [4]		
	DE binding protein 1 (TBPI).	RA Tabuchi H., Lesslauer W., Lahm H.-W., Gentz R., Brockhaus M., [5]	RP TISSUE=Placenta; PubMed=91006021; Pubmed=91006021; SEQUENCE FROM N.A. [5]		
	GN TNFRSF1A OR TNFR1 OR TNFR.	RA "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor." [6]	RP TISSUE=Placenta; PubMed=91098610; Pubmed=91098610; SEQUENCE FROM N.A. [6]		
	RN [1]_TAXID=9606;	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [7]	RP TISSUE=Placenta; PubMed=913269-3278(1990); Pubmed=913269-3278(1990); SEQUENCE FROM N.A. [7]		
	RN [1]	RA "Molecular cloning and expression of human TNF-Rs." [8]	RP TISSUE=Placenta; PubMed=91098611; Pubmed=91098611; SEQUENCE FROM N.A. [8]		
	RN [2]	RA "Molecular cloning and expression of human TNF-Rs." [9]	RP TISSUE=Placenta; PubMed=91098612; Pubmed=91098612; SEQUENCE FROM N.A. [9]		
	RN [3]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [10]	RP TISSUE=Placenta; PubMed=91351-359(1990); Pubmed=91351-359(1990); SEQUENCE FROM N.A. [10]		
	RN [4]	RA "Molecular cloning and expression of a receptor for human tumor necrosis factor 1 (TNF-R1) (P55) (CD120a) [Contains: Tumor necrosis factor receptor type I (TNFPI)]." [11]	RP TISSUE=Placenta; PubMed=91098613; Pubmed=91098613; SEQUENCE FROM N.A. [11]		
	RN [5]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [12]	RP TISSUE=Placenta; PubMed=91098614; Pubmed=91098614; SEQUENCE FROM N.A. [12]		
	RN [6]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [13]	RP TISSUE=Placenta; PubMed=91098615; Pubmed=91098615; SEQUENCE FROM N.A. [13]		
	RN [7]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [14]	RP TISSUE=Placenta; PubMed=91098616; Pubmed=91098616; SEQUENCE FROM N.A. [14]		
	RN [8]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [15]	RP TISSUE=Placenta; PubMed=91098617; Pubmed=91098617; SEQUENCE FROM N.A. [15]		
	RN [9]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [16]	RP TISSUE=Placenta; PubMed=91098618; Pubmed=91098618; SEQUENCE FROM N.A. [16]		
	RN [10]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [17]	RP TISSUE=Placenta; PubMed=91098619; Pubmed=91098619; SEQUENCE FROM N.A. [17]		
	RN [11]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [18]	RP TISSUE=Placenta; PubMed=91098620; Pubmed=91098620; SEQUENCE FROM N.A. [18]		
	RN [12]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [19]	RP TISSUE=Placenta; PubMed=91098621; Pubmed=91098621; SEQUENCE FROM N.A. [19]		
	RN [13]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [20]	RP TISSUE=Placenta; PubMed=91098622; Pubmed=91098622; SEQUENCE FROM N.A. [20]		
	RN [14]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [21]	RP TISSUE=Placenta; PubMed=91098623; Pubmed=91098623; SEQUENCE FROM N.A. [21]		
	RN [15]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [22]	RP TISSUE=Placenta; PubMed=91098624; Pubmed=91098624; SEQUENCE FROM N.A. [22]		
	RN [16]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [23]	RP TISSUE=Placenta; PubMed=91098625; Pubmed=91098625; SEQUENCE FROM N.A. [23]		
	RN [17]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [24]	RP TISSUE=Placenta; PubMed=91098626; Pubmed=91098626; SEQUENCE FROM N.A. [24]		
	RN [18]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [25]	RP TISSUE=Placenta; PubMed=91098627; Pubmed=91098627; SEQUENCE FROM N.A. [25]		
	RN [19]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [26]	RP TISSUE=Placenta; PubMed=91098628; Pubmed=91098628; SEQUENCE FROM N.A. [26]		
	RN [20]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [27]	RP TISSUE=Placenta; PubMed=91098629; Pubmed=91098629; SEQUENCE FROM N.A. [27]		
	RN [21]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [28]	RP TISSUE=Placenta; PubMed=91098630; Pubmed=91098630; SEQUENCE FROM N.A. [28]		
	RN [22]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [29]	RP TISSUE=Placenta; PubMed=91098631; Pubmed=91098631; SEQUENCE FROM N.A. [29]		
	RN [23]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [30]	RP TISSUE=Placenta; PubMed=91098632; Pubmed=91098632; SEQUENCE FROM N.A. [30]		
	RN [24]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [31]	RP TISSUE=Placenta; PubMed=91098633; Pubmed=91098633; SEQUENCE FROM N.A. [31]		
	RN [25]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [32]	RP TISSUE=Placenta; PubMed=91098634; Pubmed=91098634; SEQUENCE FROM N.A. [32]		
	RN [26]	RA "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor." [33]	RP TISSUE=Placenta; PubMed=91098635; Pubmed=91098635; SEQUENCE FROM N.A. [33]		

"Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.";
R.T. Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN [6]

R.P. SEQUENCE FROM N.A.
RN MEDLINE=9225049; PubMed=13151717;
RX Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.;
RN "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localisation to chromosome 12p13.";
RN Genomics 13:219-224(1992).
RN [7]

R.C. SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DDJB databases.
RN [8]

R.P. SEQUENCE OF 41-45.
RN MEDLINE=90110215; PubMed=2153136;
RX Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors."
RL J. Biol. Chem. 265:1531-1536(1990).
RN [9]

R.P. X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX MEDLINE=9225809; PubMed=838891;
RA Bauer D., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Lositscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445(1993).
RN [10]

R.P. X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE=97094892; PubMed=8939750;
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT "Structures of the extracellular domain of the type I tumor necrosis factor receptor."
RT Structure 4:1251-1262(1996).
RN [11]

R.P. VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
RX MEDLINE=93213501; PubMed=10198409;
RA McDermott M.F., AkSENTIEVICH I., Galon J., McDermott E.M.,
RA Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
RA Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
RA Teppo I., Wilson M., Karaslan M., Wan Y., Todd I., Wood G.,
RA Schlimgen R., Kumarajeewa T.R., Coopere S.M., Vella J.P., Amos C.I.,
RA Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
RA Hitman G.A., O'Shea J., Kastner D.L.,
RT "Germline mutations in the extracellular domains of the 55 kDa TNF receptor, TNFR1, define a family of dominantly inherited autoinflammatory syndromes.";
RT Cell 97:133-144(1999).
RL Cell 97:133-144(1999).

-!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF11/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signalling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF effects including anti-viral state and activation of the acid sphingomyelinase.

-!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONE AGGREGATED TNF RECEPTOR DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF3, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.

-!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.

-!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

-!- PTM: The soluble form is produced from the membrane form by

CC -!- DISEASE: Defect in TNFRSF1A are a cause of autosomal dominant proteolytic processing.

CC familial hibernian fever (HNF), a disease characterized by recurrent fever, abdominal pain, localized tender skin lesions and myalgia.

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -!- DATABASE: NAME=CD_PUB; NOTE=CD guide CD120a entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".

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CC DR EMBL; X55313; CA039021.1; -.

CC DR EMBL; M3294; AA03201.1; -.

CC DR EMBL; M58286; AA036755.1; -.

CC DR EMBL; M63121; AA036754.1; -.

CC DR EMBL; M7566; AA061201.1; -.

CC DR EMBL; M75864; AA061201.1; JOINED.

CC DR EMBL; M75865; AA061201.1; JOINED.

CC DR EMBL; M60275; AA036755.1; -.

CC DR EMBL; A21522; CA003201.1; -.

CC DR EMBL; BC01040; AAH10140.1; -.

CC DR PIR; A34899; GOHMTL.

CC DR PIR; A35010; A35010.

CC DR PIR; S12057; S12057.

CC DR PIR; A38208; A38208.

CC DR PDB; 1TMK; 31-JUL-94.

CC DR PDB; 1NCP; 07-DEC-95.

CC DR PDB; 1EXT; 11-JAN-97.

CC DR Genew; HGNC:1916; TNFRSF1A.

CC DR MIM: 191190; -.

CC DR InterPro; IPR00498; Death.

CC DR InterPro; IPR001568; TNFR_c6.

CC DR Pfam; PF00020; TNFR_c6; 4.

CC DR Pfam; PF00531; death; 1.

CC DR ProDom; PD00071; TNFR_c6; 1.

CC DR SMART; SNO0005; DEATH; 1.

CC DR SMART; SNO0208; TNFR; 4.

CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.

CC DR PROSITE; PS50050; TNFR_NGFR_2; 3.

CC DR PROSITE; FS50017; DEATH_DOMAIN; 1.

CC KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal; Disease mutation; Polymorphism; 3D-structure.

FT SIGNAL 1 21

FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR

FT DOMAIN 41 291 SUPERFAMILY MEMBER 1A, MEMBRANE FORM.

FT DOMAIN 22 211 TUMOR NECROSIS FACTOR B BINDING PROTEIN 1.

FT TRANSMEM 212 234 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).

FT REPEAT 43 82 TNFR-CYS 1.

FT REPEAT 83 125 TNFR-CYS 2.

FT REPEAT 126 166 TNFR-CYS 3.

FT REPEAT 167 196 TNFR-CYS 4.

FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).

FT DOMAIN 356 441 DEATH.

FT DISULFID 44 58

FT DISULFID 59 72

FT DISULFID 62 81

FT DISULFID 84 99

FT DISULFID 102 117

FT DISULFID 105 125

FT DISULFID 127 143

FT DISULFID 146 158

FT DISULFID 149 166

FT DISULFID 168 179

Query Match	100.0%	Score 941; DB 1; Length 455;
Best Local Similarity	100.0%	Pred. No. 1.2e-71; Mismatches 0; Indels 0; Gaps 0;
Matches	161; Conservative	
Qy	1 DSVCPGKTHP QNNISICCTKCHGTLYNDCPGRQDFTCREEGSFTASSENHLRHCL 60	
Db	41 DSVCPGKTHP QNNISICCTKCHGTLYNDCPGRQDFTCREEGSFTASSENHLRHCL 100	
Qy	61 SCSKCRKEMGVEISSCTVDRDTVGCRNQYHWSNLFOCNCSCLNGTVHLSQE 120	
Db	101 SCSKCRKEMGVEISSCTVDRDTVGCRNQYHWSNLFOCNCSCLNGTVHLSQE 160	
Qy	121 KQNTVCTCHAGFPLRENECVSCNSCKSLECTKLQLPQTEN 161	
Db	161 KQNTVCTCHAGFPLRENECVSCNSCKSLECTKLQLPQTEN 201	
RESULT 2		
TRIA_PIG	STANDARD; PRT; 461 AA.	
ID TRIA_PIG		
AC P5055;		
DT 01-OCT-1995 (Rel. 34, Created)		
DT 01-OCT-1996 (Rel. 34, Last sequence update)		
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60) (TNF-RI) (p55).		
GN TNFRSF1A OR TNFR1.		
OS Sus scrofa (PIG)		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Sina; Suidae; Sus.		
NCBI_TaxID 9823; [1]		
RN 1		
RP TISSUE=Kidney;		
RX MEDLINE=96011645; PubMed=7590278;		
Sutur B., Pauli U.H.; RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor."; RT receptor.";		
RL Gene 163:263-266 (1995).		
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (asparagine-specific cysteine proteases) mediating apoptosis (By similarity).		
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOPRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (By similarity).		
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.		
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.		
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CC EMBL; U19994; AAC48499.1; -		
DR HSSP; P19438; 1TNR.		
DR InterPro; IPR000498; Death.		
DR InterPro; IPR001368; TNFR_C6.		
DR Pfam; PF00020; TNFR_C6; 3.		
DR Pfam; PF00531; death; 1.		
DR Prodrom; PD000771; TNFR_C6; 1.		
DR SMART; SM00005; DEATH; 1.		
DR SMART; SM00208; TNFR_3.		
DR PROSITE; PS00652; TNFR_NGR_1; 3.		
DR PROSITE; PS00550; TNFR_NGR_2; 2.		
DR PROSITE; PS50017; DEATH_DOMAIN_1.		
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.		
FT SIGNAL 1 21		
FT CHAIN 22 461		
FT FT DOMAIN 22 210		
FT FT TRANSMEM 234 233		
FT FT REPEAT 43 82		
FT FT REPEAT 83 125		
FT FT REPEAT 126 166		
FT FT REPEAT 167 195		
FT FT DOMAIN 340 350		
FT FT DISULFID 362 447		
FT FT DISULFID 44 58		
FT FT DISULFID 59 72		
FT FT DISULFID 62 81		
FT FT DISULFID 84 99		
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FT FT DISULFID 105 125		
FT FT DISULFID 127 143		
FT FT DISULFID 146 158		
FT FT DISULFID 149 166		
FT FT DISULFID 168 179		
FT FT DISULFID 182 194		
FT FT DISULFID 185 190		
FT FT CARBOHYD 54 54		
FT FT CARBOHYD 86 86		
FT FT CARBOHYD 145 145		
FT FT CARBOHYD 151 151		
SEQUENCE 461 AA; 50696 MW; CD7361B60CD43 CRC64;		
Query Match	76.1%; Score 716 5; DB 1; Length 461;	
Matches	120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;	
Gene Similarity	77.4%; Pred. No. 5.8e-53;	
Best Local Similarity	77.4%; Pred. No. 5.8e-53;	
Qy 1 DSVCPGKTHP QNNISICCTKCHGTLYNDCPGRQDFTCREEGSFTASSENHLRHCL 60		
Db 41 ESSLCPGKTHP QNNISICCTKCHGTLYNDCPGRQDFTCREEGSFTASSENHLRHCL 100		
Qy 61 SCSKCRKEMGVEISSCTVDRDTVGCRNQYHWSNLFOCNCSCLNGTVHLSQE 120		
Db 101 SCSKCRKEMGVEISSCTVDRDTVGCRNQYHWSNLFOCNCSCLNGTVHLSQE 160		
Qy 121 KQNTVCTCHAGFPLRENECVSCNSCKSLECTKLQLPQTEN 155		
Db 161 KQNTVCTCHAGFPLRENECVSCNSCKSLECTKLQLPQTEN 194		
RESULT 3		
TRIA_MOUSE		
ID TRIA_MOUSE		
AC P25178		
STANDARD; PRT; 454 AA.		
SEQUENCE FROM N.A.		
DN 01-MAY-1992 (Rel. 22, Created)		
DT 01-MAY-1992 (Rel. 22, Last sequence update)		
DT 15-JUN-2002 (Rel. 41, Last annotation update)		
CC Tumor necrosis factor receptor superfamily member 1A precursor (p60) (TNF-RI) (p55).		
DE (TNF-RI) (TNF-RI) (p55).		
GN TNFRSF1A OR TNFR1 OR TNFR-1.		
OS Mus musculus (Mouse).		
OC Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Butteleostomi; Europygota; Metzoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.		
OC Mammalia; Butheroidea; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID 10030; RN [1] _ TaxID=10030;		
RP SEQUENCE FROM N.A.		
RX MEDLINE=9118785; PubMed=184278;		
RX Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V., RT "Cloning and expression of cDNAs for two distinct murine tumor		

RT necrosis factor receptors demonstrate one receptor is species specific.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:9128014; PubMed=1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissaneaghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.; analysis of the murine p55
 RT "Cloning, expression and cross-linking of tumor necrosis factor receptor receptor.";
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE:9203815; PubMed=1657766;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:138-140(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:9424292; PubMed=8198324;
 RA Bebo B.F., Lintilicium D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 endocheioma cell line.";
 RL Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:93156721; PubMed=8301516;
 RA Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175(1993).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Strasberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 TNFSF1/lymphotoxin-alpha. The adapter molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (By similarity).
 CC SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAF, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B ACTIVATION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CVS REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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DR EMBL; X57796; CAA40936 1; -.
 DR EMBL; I26349; AAA59361.1; -.
 DR EMBL; MT6656; AAA40465.1; -.
 DR EMBL; MB8067; AAA40465.1; JOINED.
 DR EMBL; M6655; AAA40465.1; JOINED.
 DR EMBL; BC004559; AAH04599.1; -.
 DR PIR; A3634; GQMSLT.
 DR PIR; S16677; S16677.
 DR PIR; S19021; S19021.
 DR HSSP; PI9438; IEXT.
 DR MGD; MGI-1314889; Trifksf1a.
 DR InterPro; IPR0048; Death.
 DR Pfam; PF00020; TNFR_C6.
 DR Pfam; PF00531; death_1.
 DR PRODom; PD00071; TNFR_c6_1.
 DR SMART; SM0005; DEATH_1.
 DR SMARF; SM0208; TNFR_3.
 DR PROSITE; PS00652; TNFR_NGFR_2.
 DR PROSITE; PS50017; DEATH_DOMAIN_1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR
 FT DOMAIN 22 212 SUPERFAMILY MEMBER 1A.
 FT TRANSMEM 213 235 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 236 454 POTENTIAL.
 FT REPEAT 43 82 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 83 125 TNFR-CYS 1.
 FT REPEAT 126 166 TNFR-CYS 2.
 FT REPEAT 167 196 TNFR-CYS 3.
 FT DOMAIN 339 349 TNFR-CYS 4.
 FT DISURFID 44 58 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DISURFID 59 72 DEATH.
 FT DISURFID 62 81 BY SIMILARITY.
 FT DISURFID 84 99 BY SIMILARITY.
 FT DISURFID 102 117 BY SIMILARITY.
 FT DISURFID 105 125 BY SIMILARITY.
 FT DISURFID 127 143 BY SIMILARITY.
 FT DISURFID 146 158 BY SIMILARITY.
 FT DISURFID 149 166 BY SIMILARITY.
 FT DISURFID 168 179 BY SIMILARITY.
 FT DISURFID 182 195 BY SIMILARITY.
 FT DISURFID 185 191 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC, . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC, . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC, . .) (POTENTIAL).
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 SQ SEQUENCE 454 AA; 50129 MW; 07102823C2B6D9 CRC64;

Query Match 72.3%; Score 680; DB 1; Length 454;
 Best Local Similarity 71.3%; Pred No. 6; 2e-50; Indels 0; Gaps 0;
 Matches 112; Conservative 19; Mismatches 26; Index 0;

QY 1 DSVCPQKGVHQPQNSICCTKCHGTYLYNDCPGQDTPCRCECSFTASENHLRCL 60
 Db 41 DSCLPQKGKVHSKNSICCTKCHGTYLYVSDCPSPGRDTVCRECKGFTASONYRLQCL 100

QY 61 SOSKRKEMQVQLSSTCVDRTVCGRKQYRHWSNLQFCFNCSLCLNGTVHLSQBE 120
 Db 101 SCKTCRKEMQVQLSSTCVDRTVCGRKQYRHWSNLQFCFNCSLCLNGTVHLSQBE 160

QY 121 KONTVCTCHAGFFLRENECNSCSNCKSLETKCHGTYLYVSDCPSPGRDTVCRECKGFTASONYRLQCL 157

Db 161 TQNTVCNCHAGFFLRESECVPSCSHCKNNBECMKLCLP 197

RESULT 4
 TRIA_BOVIN ID TRIA_BOVIN STANDARD: PRT; 471 AA.
 AC 019131;

DT	16-OCT-2001 (Rel. 40; Created)	FT	DISULFID	84	99	BY SIMILARITY.
DT	16-OCT-2001 (Rel. 41; Last sequence update)	FT	DISULFID	102	117	BY SIMILARITY.
DT	15-JUN-2002 (Rel. 41; Last annotation update)	FT	DISULFID	105	125	BY SIMILARITY.
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60) (TNF-RI) (TNF-RI) (p55).	FT	DISULFID	127	143	BY SIMILARITY.
GN	TNFRSF1A OR TNFR1.	FT	DISULFID	146	158	BY SIMILARITY.
OS	Bos taurus (Bovine).	FT	DISULFID	149	166	BY SIMILARITY.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Chordiiodactyla; Ruminantia; Pecora; Bovoidea; Bosidae; Bovinae; Bos.	FT	DISULFID	168	179	BY SIMILARITY.
OC	OCBII-TaxID:9913;	FT	DISULFID	182	194	BY SIMILARITY.
RN	[1]	RP	SEQUENCE N.A.	185	190	BY SIMILARITY.
RN	RC TISSUE:Aorta;	RP	SEQUENCE N.A.	190	194	BY SIMILARITY.
RX	MEDLINE:982373505; PubMed:9613449;	RT	Lee E.-K., Kehrt M.E. Jr., Taylor M.J. / "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor (TNF)-receptor I.";	71.7%	Score 674.5;	DB 1; Length 471;
RA	RT	CC FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signalling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (apartase-specific cysteine proteases) mediating apoptosis (By similarity). CC - SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (By similarity).	Query Match Best Local Similarity 71.6%; Pred. No. 1.8e-19; Matches 111; Conservative 17; Mismatches 26; Indels 1; Gaps 1;			
CC	-!- SIMILARITY: CONTAINS 4 TNFR CYTS REPEATS.	Qy	1 DSYVCPQKVIHPQNNSICCTCKHGTYLYNDCPGPQDTDRECGSGSFASENHLRHCL 60			
CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.	Db	41 EFPVCPQKVNIPQNNSICCTCKHGTYLYNDCPGPQDTDRCRVAPGTVTALENHLRRCL 100			
CC	CC	Qy	61 SCSKCRKEMGOVIEISSSTVDITVCCRNKQHYWSENLFQCFNCSLCLNGTVHLSQEE 120			
CC	CC	Db	101 SCSRCRDEMFLQVEISPCVQDVIDTVCCRNQREYWGEGTFRCLNCSLCNGTVNPQEE 160			
CC	CC	Qy	121 KONTVCTCHAGFELRENEUCCSNCKKSLEETKL 155			
CC	CC	Db	161 RDTTICHMGMFFLKGAKCITSCHDRNK-ECEKL 194			
CC	CC	CC	RESULT 5			
CC	CC	CC	ID TR1A_RAT STANDARD; PRT; 461 AA.			
CC	CC	CC	AC P22934; Q91V30; Q91V33;			
CC	CC	CC	DT 01-AUG-1991 (Rel. 19; Created)			
CC	CC	CC	DT 01-MAR-1992 (Rel. 21; Last sequence update)			
CC	CC	CC	DT 15-JUN-2002 (Rel. 41; Last annotation update)			
CC	CC	CC	DE Tumor necrosis factor receptor superfamily member 1A precursor (p60) use (TNF-RI) (TNF-RI) (p55).			
CC	CC	CC	DE TNFRSF1A OR TNFR1 OR TNFR-1.			
CC	CC	CC	OS Rattus norvegicus (Rat).			
CC	CC	CC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Ratus.			
CC	CC	CC	NCBI TaxID:10116;			
CC	CC	CC	RN [1]			
CC	CC	CC	RN SEQUENCE FROM N.A.			
CC	CC	CC	RX MEDLINE=91090841; PubMed=1702293;			
CC	CC	CC	RA Himmerl A.; Maurer-Poggy I.; Kroenke M.; Scheuerich P.; Pfizenmaier K.,			
CC	CC	CC	RA Lantz M.; Olsson I.; Haupmann R.; Stratowa C.; Adolf G.R.;			
CC	CC	CC	RA RT Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";			
CC	CC	CC	RT DNA Cell Biol. 9:705-715(1990).			
CC	CC	CC	RN [2]			
CC	CC	CC	RN SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.			
CC	CC	CC	RC STRAIN=Various;			
CC	CC	CC	RA Furuya T.; Salstrom J.L.; Bina J.; Hashimamoto A.; Dobbins D.E., Wilder R.L.; Reimers E.P.;			
CC	CC	CC	RT RT Polymorphisms of the tumor necrosis factor receptor type 1 locus among autoimmune susceptible and resistant inbred rat strains.";			
CC	CC	CC	RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
CC	CC	CC	CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homomeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signalling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity).			
CC	CC	CC	CC - SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO			

CC	TNFR COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).	Db	41 DNLCQPGKVAHPKRNSCTCKHGKVLYSHCOPSPQETVECVNGKTFIASQHVRQL
CC	-!- SUBCELLULAR LOCATION: TYPE I membrane protein.	Qy	61 SCCRCKENGQFVIISSCTVDRDVCGCRKQYRHYSNLIQCFNCISLICNGTVHLSQE
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.	Db	101 SCKTRKEMFQVEISPKADMDTVCGGKKNQFORYLSBTHQCVDSPCPNGTIPKE
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Qy	121 KQNVTCGHAGFFLRENECVSNCKSLETKLQPQIEN 161
CC	-----	Db	161 KQNTVCNCHAGFFLSGNBTCPSCSHCKNQECMVKLCLPPVAN 201
CC	-----	-----	-----
CC	-----	RESULT 6	-----
CC	-----	TR23_MOUSE	-----
DR	ID TR23_MOUSE STANDARD; PRT; 176 AA.	ID TR23_MOUSE	-----
DR	AC Q9E63; O8VHO0;	AC Q9E63; O8VHO0;	-----
DR	DT 15-JUN-2002 (Rel. 41, Last sequence update)	DT 15-JUN-2002 (Rel. 41, Last sequence update)	-----
DR	EMBL AF329971; ARK53562.1; -.	EMBL AF329971; ARK53562.1; -.	-----
DR	EMBL AF329971; ARK53563.1; -.	EMBL AF329971; ARK53567.1; -.	-----
DR	EMBL AF329978; ARK53564.1; -.	EMBL AF329979; ARK53565.1; -.	-----
DR	EMBL AF329980; ARK53566.1; -.	PIR; B3555; B36555.	-----
DR	HSSP; PI9438; INCR.	DR Domains; PS00050; DEATH_1.	-----
DR	InterPro; IPR000488; Death.	DR PROSITE; PS00652; TNFR_C6.	-----
DR	InterPro; IPR001368; TNFR_C6.	DR PROSITE; PS0050; TNFR_c6; 4.	-----
DR	Pfam; PF00531; death; 1.	DR PRODom; PD000771; TNFR_c6; 1.	-----
DR	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	DR SMART; SM0005; DEATH_1.	-----
FT	SIGNAL 1	FT SIGNAL 1	-----
FT	CHAIN 22	FT CHAIN 22	-----
FT	461	461	-----
FT	TUMOR_NECROSIS_FACTOR_RECECTOR_SUPERFAMILY_MEMBER_1A.	TUMOR_NECROSIS_FACTOR_RECECTOR_SUPERFAMILY_MEMBER_1A.	-----
FT	SUPERFAMILY MEMBER_1A.	SUPERFAMILY MEMBER_1A.	-----
FT	EXTRACELLULAR (POTENTIAL).	EXTRACELLULAR (POTENTIAL).	-----
FT	POTENTIAL.	POTENTIAL.	-----
FT	DOMAIN 22	DOMAIN 22	-----
FT	211	211	-----
FT	TRANSMEM 212	TRANSMEM 212	-----
FT	234	234	-----
FT	DOMAIN 235	DOMAIN 235	-----
FT	461	461	-----
FT	CYTOSPLIC (POTENTIAL).	CYTOSPLIC (POTENTIAL).	-----
FT	TNF-CYS 1.	TNF-CYS 1.	-----
FT	TNF-CYS 2.	TNF-CYS 2.	-----
FT	REPEAT 83	REPEAT 83	-----
FT	126	126	-----
FT	166	166	-----
FT	196	196	-----
FT	REPEAT 167	REPEAT 167	-----
FT	196	196	-----
FT	REPEAT 344	REPEAT 344	-----
FT	354	354	-----
FT	DEATH_1	DEATH_1	-----
FT	448	448	-----
FT	DOMAIN 363	DOMAIN 363	-----
FT	448	448	-----
FT	DEATH.	DEATH.	-----
FT	BY SIMILARITY.	BY SIMILARITY.	-----
FT	DISULFID 44	DISULFID 44	-----
FT	72	72	-----
FT	DISULFID 59	DISULFID 59	-----
FT	81	81	-----
FT	DISULFID 84	DISULFID 84	-----
FT	99	99	-----
FT	DISULFID 102	DISULFID 102	-----
FT	117	117	-----
FT	125	125	-----
FT	DISULFID 105	DISULFID 105	-----
FT	123	123	-----
FT	143	143	-----
FT	158	158	-----
FT	DISULFID 146	DISULFID 146	-----
FT	166	166	-----
FT	DISULFID 149	DISULFID 149	-----
FT	166	166	-----
FT	DISULFID 168	DISULFID 168	-----
FT	179	179	-----
FT	DISULFID 182	DISULFID 182	-----
FT	195	195	-----
FT	DISULFID 185	DISULFID 185	-----
FT	191	191	-----
FT	BY SIMILARITY.	BY SIMILARITY.	-----
FT	CARBONYD 54	CARBONYD 54	-----
FT	151	151	-----
FT	DISULFID 151	DISULFID 151	-----
FT	201	201	-----
FT	DISULFID 201	DISULFID 201	-----
FT	230	230	-----
FT	VARIANT 230	VARIANT 230	-----
FT	I -> V (IN STRAINS LEW_NHSD, ACI/SEGHSID, DA_BKL AND F34/NHSD).	I -> V (IN STRAINS LEW_NHSD, ACI/SEGHSID, DA_BKL AND F34/NHSD).	-----
FT	H -> P (IN STRAINS LEW_NHSD, ACI/SEGHSID, DA_AKL, F34/NHSD AND BN_SSNHSD).	H -> P (IN STRAINS LEW_NHSD, ACI/SEGHSID, DA_AKL, F34/NHSD AND BN_SSNHSD).	-----
SQ	SEQUENCE 461 AA;	SEQUENCE 461 AA;	-----
SQ	50969 MN;	50969 MN;	-----
SQ	EB23C05450FB0202 CRC64;	EB23C05450FB0202 CRC64;	-----
QY	Query Match Score 71.1%; Best Local Similarity 68.3%; Matches 110; Variant 110; Consecutive 18; Mismatches 33; Indels 0; Gaps 0;	QY Score 66.9%; Pred. No. 5.2e-49; Matches 68; Variant 68; Consecutive 18; Mismatches 33; Indels 0; Gaps 0;	-----
QY	1 DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCGPQGDTCRCESGSFTASENHRLHCL 60	QY 1 DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCGPQGDTCRCESGSFTASENHRLHCL 60	-----

FT	DISULFID	93	106	BY SIMILARITY.
FT	DISULFID	96	114	BY SIMILARITY.
FT	DISULFID	116	131	BY SIMILARITY.
FT	DISULFID	134	147	BY SIMILARITY.
FT	DISULFID	137	155	BY SIMILARITY.
FT	CARBOHID	148	148	N-LINKED (GLCNAC. . .) (POTENTIAL).
SC	SEQUENCE	176 AA;	19594 MW:	EE30D617749DBB7 CRC64;
Query Match		21.3%	Score 200.5;	DB 1; Length 176;
Best Local Similarity	33.8%;	Pred. No.	2.4e-10;	
Matches	42; Conservative	16;	Mismatches	60;
Indels	7;	Gaps	4;	
Qy	4 CPQGKYTHPQNSICCTKCHKGTYLYNDCPGQDPTDCRECBGSFTASENHURHCLSCS	63	RL	Curr. Biol. 6:1669-1676 (1996).
Db	38 CPDGEBY--QSNDVCKTKPSGTFKAPCKLIPHTQSQCERCPENFTGDNHDCELCS	94	RN	[5]
Qy	64 KCRKENGQVEISCTYDRDTVCGCRKNQYRHYSENLFQCFNCISLCLNG-TWHSQEQKQ	122	RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
Db	95 TCDKDQNMY-.ADCSATSDRKCECQIGLY-YDPKFPESCRPCTKCPQSIPIVNLQECNSTA	151	RX	MEDLINE=9727273; PubMed=9114039;
Qy	123 NTVCST 1.27		RA	Se創ton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.T.,
Db	152 NTVCSt 156		RT	"LARD: a new lymphoid specific death domain containing receptor regulated by alternative pre-mRNA splicing."
RESULt 7			RT	PROC. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
TR12_HUMAN	STANDARD; PRT; 417 AA.		RL	RN [6].
ID	Q93036; Q93137; Q92983; P78515; Q99722; P78507;		RN	SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
AC	Q99830; Q9BY86; O14865; O14866; O00275; O00277; O00278;		RX	MEDLINE=98113360; PubMed=9446802;
AC	O00280; Q9UNEO; Q9UMEI;		RA	Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B., Sales G.;
DT	01-NOV-1997 (Rel. 35, Created)		RT	"A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas;"
DT	01-NOV-1997 (Rel. 35, Last sequence update)		RT	Biophys. Res. Commun. 242:376-379 (1998).
DT	15-JUN-2002 (Rel. 41, Last annotation update)		RP	SEQUENCE FROM N.A. (ISOFORM 1).
DE	Tumor necrosis factor receptor superfamily member 12 precursor (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-mediating receptor TRAMP) (Death domain receptor 3) (WSL protein) (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated receptor of death) (LARD).		RA	Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E., Hayashi S., Sato M., Shiozawa K., Tsukano Y.;
GN	TNFRSF12 OR WSL1 OR WSL OR APO3 OR DDR3.		RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
OS	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.		RN	[7].
OC			RN	SEQUENCE FROM N.A. (ISOFORM 1).
MM			RN	RA, Wilson A., French L.E., Hofmann K., Steiner V., Bodmer J.-L., Burns K., Schneider P., Schroeter M., Wilson A., French L.E., Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E., Browning J.B., Macdonald H.R., Tschoopp J., RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95).";
NCBI_TaxID	9606;		RT	to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95).";
RN	[1]		RL	Immunity 6:79-88(1997).
RP	SEQUENCE OF 4-417 FROM N.A.		RN	[9].
RC	SEQUENCE OF 7-417 FROM N.A.		RP	SEQUENCE OF 7-417 FROM N.A.
RC	TISSUE=Brain;		RC	RC TISSUE=Brain;
RA	Chaudhary P.M., Hood L.E.;		RA	RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL	-: FUNCTION: Receptor for TNFSF12/APO3/L/TWEAK. Interacts directly with the adaptor TRADD. Mediates activation of NF-kappaB and induces apoptosis. May play a role in regulating lymphocyte homeostasis.		CC	-: FUNCTION: Receptor for TNFSF12/APO3/L/TWEAK. Interacts directly with the adaptor TRADD. Mediates activation of NF-kappaB and induces apoptosis. May play a role in regulating lymphocyte homeostasis.
CC	-: SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNRF1 RECEPTOR TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING		CC	-: SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNRF1 RECEPTOR TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING
CC	-: SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)		CC	-: SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
CC	(Potential).		CC	(Potential).
CC	-: ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE), 2/LARD-1B, 3/WSL-S1/LARD-1, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11, 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND 12/BETA SOUBLE; ARE PRODUCED BY ALTERNATIVE SPlicing.		CC	-: ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE), 2/LARD-1B, 3/WSL-S1/LARD-1, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11, 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND 12/BETA SOUBLE; ARE PRODUCED BY ALTERNATIVE SPlicing.
CC	-: TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOcyTES; DETECTED IN LYMPHOcyTE-RICH TISSUES SUCH AS THYMUS, COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.		CC	-: TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOcyTES; DETECTED IN LYMPHOcyTE-RICH TISSUES SUCH AS THYMUS, COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC	-: PIM: GLYCOSylATED (PROBABLY).		CC	-: PIM: GLYCOSylATED (PROBABLY).
CC	-: SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.		CC	-: SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-: CAUTION: Ref. 5 reports isoform 1 DEATH DOMAIN.		CC	-: CAUTION: Ref. 5 reports isoform 1 DEATH DOMAIN.
CC	-: CAUTION: Ref. 5 reports isoform 4 at position 208 a serine residue instead of arginine.		CC	-: CAUTION: Ref. 5 reports isoform 4 at position 208 a serine residue instead of arginine.
CC	[3].		CC	[3].
RP	SEQUENCE FROM N.A.		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;		CC	DR EMBL: Y09332; CAA70561.1;
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.		DR	DR EMBL: Y09332; CAA70559.1;
RN	[4].		DR	DR EMBL: Y09332; CAA70560.1;
RP	SEQUENCE FROM N.A. (ISOFORM 1).		DR	DR EMBL: U72763; AAC50819.1;
RC	TISSUE=Heart;		DR	DR EMBL: U72763; AAC50819.1;
RX	MEDLINE=97148200; PubMed=8934832;		DR	DR EMBL: U72763; AAC50819.1;
RA	Marsden S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Bauer K.D., Asikkeneni A.;		DR	DR EMBL: Y09332; CAA70559.1;
RT	"Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kappa-B.";		DR	DR EMBL: U72763; AAC50819.1;

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshash-Borisi A., Yoshida K., Hassegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.; Nature 409:685-690 (2001).
-1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-1- TISSUE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.

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EMBL; AJ2798265; CAC76406_1; -.
EMBL; AJ276505; CAC7353_1; -.
EMBL; AY046551; AAU05073_1; -.
EMBL; AK012838; BAB28502_1; -.
HSRP; P19438; IBEKT.
MGI; MGI:1930270; Infres22.
InterPro; IPR001368; TNFR_C6.
PFam; PF00020; TNFR_C6_3.
SMART; SM00208; TNFR_3.
PROSITE; PS00632; TNFR_NGFR_1; FALSE_NEG.
PROSITE; PS00502; TNFR_NGFR_2; 2.
Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
DOMAIN; 1 20 CYTOPLASMIC (POTENTIAL); Membrane PROTEIN
TRANSMEM 21 41 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
DOMAIN; 42 180 EXTRACELLULAR (POTENTIAL).
REPEAT; 47 82 TNFR-CYS 1.
REPEAT; 84 124 TNFR-CYS 2.
REPEAT; 125 165 TNFR-CYS 3.
DISULFID; 48 59 BY SIMILARITY.
DISULFID; 60 73 BY SIMILARITY.
DISULFID; 63 82 BY SIMILARITY.
DISULFID; 85 100 BY SIMILARITY.
DISULFID; 103 116 BY SIMILARITY.
DISULFID; 106 124 BY SIMILARITY.
DISULFID; 126 141 BY SIMILARITY.
DISULFID; 144 157 BY SIMILARITY.
DISULFID; 147 165 BY SIMILARITY.
CARBOHYD; 62 62 N-LINKED (GLCNAC, . .) (POTENTIAL).
CARBOHYD; 158 158 N-LINKED (GLCNAC, . .) (POTENTIAL).
CONFLICT; 12 12 L -> V (IN REF. 3).
CONFLICT; 171 180 RRSVANVPI -> NPNRFLFL (IN REF. 2).
SEQUENCE; 180 AA; 20226 MW; FIF56E165ADD53FA CRC64; 4;

Query Match 21.1%; Score 198.5; DB 1; Length 180;
Best Local Similarity 32.8%; Pred. No. 3.6e-10;
Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;

4 CPOQGYIHPQNNSCCTKCHKGTYLYNNGCPGFCQDTDORECGSFTASENHILRHCLSCS 63
48 CPAGPEVKEISSLSTVDRTVCGERKRNQYRHWSENDFQCFNCNSLCLNLNG-TVHUSQCERQ 122
64 KCRKEMGQVEISSLSTVDRTVCGERKRNQYRHWSENDFQCFNCNSLCLNLNG-TVHUSQCERQ 122
105 TCDD--QEMVADCSATSDRKCQCRTGly-YDPKFPESCRPTKCPQGIPVLCBNCNSTA 161
123 NTVCT 127
162 NTVC5 166

FT	CHAIN	31	435	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 3.	CC	-!- SUBCELLULAR LOCATION: Typ I membrane protein.
FT	DOMAIN	31	227	EXTRACELLULAR (POTENTIAL).	CC	-!- PTM: N- AND O-glycosylated.
FT	TRANSMEM	228	248	POTENTIAL.	CC	-!- PROTEIN: Phosphorylated on serine residues.
FT	DOMAIN	249	435	CYTOPLASMIC (POTENTIAL).	CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
FT	REPEAT	42	81	TNFR-CYS 1.	CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
FT	REPEAT	82	124	TNFR-CYS 2.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	REPEAT	125	168	TNFR-CYS 3.	CC	-----
FT	REPEAT	169	211	TNFR-CYS 4.	CC	-----
FT	DISULFID	43	58	BY SIMILARITY.	CC	-----
FT	DISULFID	59	72	BY SIMILARITY.	CC	-----
FT	DISULFID	62	80	BY SIMILARITY.	CC	-----
FT	DISULFID	83	98	BY SIMILARITY.	CC	-----
FT	DISULFID	101	116	BY SIMILARITY.	CC	-----
FT	DISULFID	104	124	BY SIMILARITY.	CC	-----
FT	DISULFID	126	132	BY SIMILARITY.	CC	-----
FT	DISULFID	139	148	BY SIMILARITY.	CC	-----
FT	DISULFID	142	167	BY SIMILARITY.	CC	-----
FT	DISULFID	170	185	BY SIMILARITY.	CC	-----
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-----
FT	SEQUENCE	177	177	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-----
SQ	435 AA;	467-09 MW;	62465E6202F656F	CRC64;	DR	EMBL; M34761; AAB9544.1; -.
Query Match	19.9%; Score 187.5; DB 1; Length 435; Best Local Similarity 32.0%; Pred. No. 6.2e-09; Mismatches 71; Indels 13; Gaps 7; Matches 49; Conservative 17; MisMatches 71; Indels 13; Gaps 7;	DR	PIR; A2518; Q0HUN.			
Qy	8 KYVHPONNSICCTKCHKGTYLYNDCPGPQDTCREBEGSTASENHLRHCSCSKCRK 67	DR	HSSP; P0174; INGR.			
Db	49 EYVBPQRH-ICCSRCPGPTVSAKC-SRIRDTVCATGAENSYNEHWMLYTQCLRPCDP 106	DR	Genew; HGNC; 7809; NGFR.			
Qy	68 EMGQVEISSLCTVDRDTVGCRKRQHWSENLFQFCNSL--CUNGTVHLSQC--KQ 122	DR	MIM; 162010; -.			
Db	107 VMGHEELAPCTSRSKTPCQRCMCAAWA--LECTHCELLSDCPGTEABLKOEVGKG 163	DR	InterPro; IPR00498; Death.			
Qy	123 NTVCTI-CHAGFFERENECSVCSGKSKLEC 151	DR	InterPro; IPR001348; TNFR_c6.			
Db	164 NNHCVPCKAGHF-QNTSSPSARCPQPHTRC 191	DR	Pfam; PF0020; TNFR_C6; 4.			
RESULT 10		DR	SMART; SM0005; DEATH; 1.			
TRI6_HUMAN	STANDARD;	DR	SMART; SM0208; TNFR; 3.			
ID	P08138;	DR	PROSTE; PS50050; TNFR_NGFR; 1; 3.			
AC	01-AUG-1988 (Rel. 08, Created)	DR	PROSTE; PS50052; TNFR_NGFR; 2; 4.			
DT	01-AUG-1988 (Rel. 08, Last sequence update)	DR	PROSTE; PS50017; DEATH_DOMAIN; 1.			
DT	16-OCT-2001 (Rel. 40, Last annotation update)	DR	Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein; SIGNAL			
DE	Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGFR p75NTR) (p75 ICO) (Low affinity neurotrophin receptor p75NTR).	FT	FT			
GN	(p75 ICO) (Low affinity neurotrophin receptor p75NTR).	FT	FT			
OS	Homo sapiens (Human)	FT	FT			
OC	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo; OX; NCBI_TaxID=9606;	FT	FT			
RN	[1]	FT	FT			
RP	SEQUENCE FROM N.A.	FT	FT			
MEDLINE-87051725; PubMed=3022937;	FT	FT	FT			
Johnson D., Lanahan A., Sebagh A., Morgan C., Mercer E., Bothwell M., Chao M.; Expression and structure of the human NGF receptor.; Cell 47:545-554 (1986).	FT	FT	FT			
RN [2]	SEQUENCE OF 1-22 FROM N.A.	FT	FT			
MEDLINE-89096903; PubMed=2850481;	FT	FT	FT			
RA	Senhal A., Patil N., Chao M.; A constitutive promoter directs expression of the nerve growth factor receptor gene.; Mol. Cell. Biol. 8:3160-3167(1988).	FT	FT			
CC	-- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells.	FT	FT			
CC	-- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-	FT	FT			
SQ	SEQUENCE	427 AA;	45183 MW;	B09FA43FB3D625B CRC64;	CC	associated cell death executor.
Query Match	19.4%; Score 182.5; DB 1; Length 427; Best Local Similarity 32.1%; Pred. No. 1.6e-08; Mismatches 62; Indels 23; Gaps 11; Matches 52; Conservative 25; MisMatches 62; Indels 23; Gaps 11;	CC	-!- PTM: N- AND O-glycosylated.			
Qy	4 CPOGVVYHPPONNSICCTKCHKGTYLYNDCPGPQDTCREBEGSTASENHLRHCSC 62	CC	-!- PROTEIN: Phosphorylated on serine residues.			
Db	32 CPTGVLTH--SGCCAKAGNLGEVAQPC-GANQ-TYCEPCLSVTSVSDVWATEPKPC 86	CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
Qy	63 SKCRKEMGQVEISSLCTVDRDTVGCRKRQHWSENLFQFCNSL--CUNGTVHLSQC 120	CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
Db	87 TEC--VGLOMSAQCVAEADAVRC--AIGYQDERTGRCEACRVCEAGSGLVFSQD 140	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
Qy	121 KQNTVC-TCHAGFFERENECSVCSN--KKSLECTK 153	CC	-----			

Matches	51;	Conservative	19;	Mismatches	67;	Indels	49;	Gaps	7;	
Qy	13 QNSNICCTKCHRGTYLYNDPCPGDPTDCREGESESGFTASAPENHLRHCLSC-SKCKRKEMGQ	71								
Db	34 EKDGLCCTSCPGSYASRLC-GPGSDIVCSPPKNETETASTNHAPCVSQRGRCGHLS-	91								
Qy	72 VELISCTYDRDTVGCRKNOY-----	92								
Db	92 -EQQSCDQTRDVCDCSAGNYCILKGEOGCRICAPAKTKCPAGYGSGHTRTDGYLCTKCP	150								
Qy	93 RHYWSENLFQCNCSLCLNG-TVHLSQEKGKONTVTCAGAFFFRLRNECYCSNCNKSLLBC	151								
Db	151 RYTYSDAVSSTTCTSSFNYTISVEFNLYPYNDTSCTTTAG---PNEVVKTSFSVTLNH	206								
Qy	152 TKLCLP 157									
Db	207 TD-CDP 211									
RESULT 14										
VT2_SFVKA	STANDARD;	PRT;	325 AA.							
AC	P25943; P25943; P25943;									
DT	01-MAY-1992 (Rel. 22, Created)									
DT	01-MAY-1992 (Rel. 22, Last sequence update)									
DT	15-JUN-2002 (Rel. 41, Last annotation update)									
DE	Tumor necrosis factor soluble receptor precursor (Protein T2).									
GN										
OS	Shope fibroma virus (strain Kasza) (SFV).									
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;									
OC	Leporipoxvirus.									
OC	NCBI_TaxID=10272;									
RN										
RP	SEQUENCE FROM N.A.									
RX	MEDLINE=87321103; PubMed=2820128;									
RA	Upton C., Delange A.M., McFadden G.;									
RA	"Tumorigenic poxviruses: Genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome." (See http://www.isb-sib.ch/announce/11.html .)									
RT	Virology 160:20-30(1987).									
RL										
RN										
RP	FUNCTION.									
RX	MEDLINE=91207415; PubMed=1850261;									
RA	Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., Goodwin R.G.									
RA	"T2 open reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor."									
RT	Biochem. Biophys. Res. Commun. 176:335-342 (1991)									
RL	-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPLIFYING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.									
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.									
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/11.html .)									
CC	EMBL; M17433; ; NOT_ANNOTATED_CDS.									
DR	EMBL; A23727; CAA01687.1; -.									
DR	PIR; B43692; B43692.									
DR	HSSP; P19438; IEX7.									
DR	Fam: P00020; TNFR_C6; 2.									
DR	ProDom; PDB00771; TNFR_C6; 1.									
DR	SMART; SM00208; TNFR_C6; 3.									
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.									
DR	PROSITE; PS00650; TNFR_NGFR_2; 1.									
KW	Receptor; Glycoprotein; Repeat; Signal.									
FT	SIGNAL_1									
FT	POTENTIAL.									
CHAIN	17	325								

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DR; M17433; ; NOT_ANNOTATED_CDS.

EMBL; A23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; IEX7.

Fam: P00020; TNFR_C6; 2.

ProDom; PDB00771; TNFR_C6; 1.

SMART; SM00208; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Repeat; Signal.

SIGNAL_1

POTENTIAL.

CHAIN

17

325

TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.

FUNCTION.

MEDLINE=91207415; PubMed=1850261;

Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., Goodwin R.G.

"T2 open reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor."

Biochem. Biophys. Res. Commun. 176:335-342 (1991)

-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPLIFYING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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DR; M17433; ; NOT_ANNOTATED_CDS.

EMBL; A23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; IEX7.

Fam: P00020; TNFR_C6; 2.

ProDom; PDB00771; TNFR_C6; 1.

SMART; SM00208; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Repeat; Signal.

SIGNAL_1

POTENTIAL.

CHAIN

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DR; M17433; ; NOT_ANNOTATED_CDS.

EMBL; A23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; IEX7.

Fam: P00020; TNFR_C6; 2.

ProDom; PDB00771; TNFR_C6; 1.

SMART; SM00208; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Repeat; Signal.

SIGNAL_1

POTENTIAL.

CHAIN

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TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.

FUNCTION.

MEDLINE=91207415; PubMed=1850261;

Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., Goodwin R.G.

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-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPLIFYING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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DR; M17433; ; NOT_ANNOTATED_CDS.

EMBL; A23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; IEX7.

Fam: P00020; TNFR_C6; 2.

ProDom; PDB00771; TNFR_C6; 1.

SMART; SM00208; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Repeat; Signal.

SIGNAL_1

POTENTIAL.

CHAIN

17

325

TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.

FUNCTION.

MEDLINE=91207415; PubMed=1850261;

Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., Goodwin R.G.

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-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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or send an email to license@sb-sib.ch.

DR; M17433; ; NOT_ANNOTATED_CDS.

EMBL; A23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; IEX7.

Fam: P00020; TNFR_C6; 2.

ProDom; PDB00771; TNFR_C6; 1.

SMART; SM00208; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Repeat; Signal.

SIGNAL_1

POTENTIAL.

CHAIN

17

325

TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.

FUNCTION.

MEDLINE=91207415; PubMed=1850261;

Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., Goodwin R.G.

"T2 open reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor."

Biochem. Biophys. Res. Commun. 176:335-342 (1991)

-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPLIFYING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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or send an email to license@sb-sib.ch.

DR; M17433; ; NOT_ANNOTATED_CDS.

EMBL; A23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; IEX7.

Fam: P00020; TNFR_C6; 2.

ProDom; PDB00771; TNFR_C6; 1.

SMART; SM00208; TNFR_C6; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00650; TNFR_NGFR_2; 1.

Receptor; Glycoprotein; Repeat; Signal.

Page 14

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KW	DR
Receptor; Apoptosis;	PROSTATE; PSO0050; TNFR-NKG2; 2.
SIGNAL	DEATH DOMAIN; 1.
CHAIN	TUMOR NECROSIS FACTOR RECEPTOR
FT	SUPERFAMILY MEMBER 6.
DOMAIN	EXTRACELLULAR (POTENTIAL).
TRANSMEM	CYTOSPLICMIC (POTENTIAL).
FT	POTENTIAL.
DOMAIN	TNFR-CVS 1.
REPEAT	TNFR-CVS 2.
FT	TNFR-CVS 3.
REPEAT	DEATH.
FT	BY SIMILARITY.
DOMAIN	BY SIMILARITY.
DISULPID	BY SIMILARITY.
FT	BY SIMILARITY.
DISULPID	BY SIMILARITY.
FT	BY SIMILARITY.
DISULPID	BY SIMILARITY.
FT	BY SIMILARITY.
DISULPID	BY SIMILARITY.
FT	BY SIMILARITY.
DISULPID	BY SIMILARITY.
FT	BY SIMILARITY.
DISULPID	BY SIMILARITY.
FT	N-LINKED (GLCNAC, -) (POTENTIAL).
CARBHYD	N-LINKED (GLCNAC, -) (POTENTIAL).
SEQUENCE	332 AA; 37592 MW; 5B8B3682756BFB CRC64;

	Best Local Matches	Similarity	Conservative	Pred.	Indels	Gaps	4
Qy	1 DSVPQGKVIPHQNNSICCTKCHGTYLYNDCEPGQDTCRBCESG-SFTASENHLRC	29.1%	18;	Mismatches			
Db	4.3 ESECPGQH--RSQFCCPCCPGKRRKHDCTSPPGAQCPVCSGBDVTDPKNHSSKC	59	0	No. 4.1E-08;	65;		
Qy	60 LSCSKCRKENGQVELTSCTWDRDTVGGERKRNQYRHYSWENLFOCFNLSCLCNGTVHLSQ	99	119				
Db	100 RRCRVGDEHGLEVKNCTRTQNTKCRCKENFFCH--TSQCEHONPCTCERGVIE-NCT	156	120	EKQNTVC	126		
Qy	157 PTSNPKC	163					

Search completed: December 3, 2002, 14:40:24
Job time : 15 secs

ALIGNMENTS							
RESULT 1							
1: sp_eukarya:*							
2: sp_bacteria:*							
3: sp_fungi:*							
4: sp_human:*							
5: sp_invertebrate:*							
6: sp_mammal:*							
7: sp_mbrc:*							
8: sp_organelle:*							
9: sp_phage:*							
10: sp_plant:*							
11: sp Rodent:*							
12: sp_virus:*							
13: sp_vertebrate:*							
14: spUnclassified:*							
15: sp_rvirus:*							
16: sp_bacteriav:*							
17: sp_archeap:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description	Score	Match Length DB ID
1	780	82.9	446	6	Q95ND3	Q95ND3 Felis silve	Q95ND3
2	756	90.3	189	6	Q97530	097530 canis famili	Q97530
3	731	77.7	413	11	Q95185	Q95185 felis silve	Q95185
4	202	21.5	413	11	Q99MM1	Q99MM1 mus musculu	Q99MM1
5	193	20.5	387	13	Q9PVD4	Q9PVD4 xenopus lae	Q9PVD4
6	191	20.3	433	11	Q91ZM6	Q91ZM6 rattus norv	Q91ZM6
7	188	20.0	302	13	Q9PU50	Q9PU50 salvelinus	Q9PU50
8	182	5.5	285	13	Q9DGH7	Q9DGH7 Gallus gall	Q9DGH7
9	179	5.5	19.1	357	Q9DD34	Q9DD34 brachydano	Q9DD34
10	176	5.5	18.8	320	Q9D079	Q9D079 cowpox viru	Q9D079
11	175	18.7	459	11	Q62327	Q62327 mus musculu	Q62327
12	175	5.5	312	13	Q9DGH8	Q9DGH8 gallus gall	Q9DGH8
13	175	5.5	322	12	Q72761	Q72761 cowpox viru	Q72761
14	171	5.5	18.2	316	Q57092	Q57092 ectromelia	Q57092
15	171	5.5	18.2	320	Q57091	Q57091 ectromelia	Q57091
16	171	5.5	18.2	320	Q57300	Q57300 ectromelia	Q57300
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22	171	5.5	18.2	320	Q57306	Q57306 ectromelia	Q57306
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31	171	5.5	18.2	320	Q57315	Q57315 ectromelia	Q57315
32	171	5.5	18.2	320	Q57316	Q57316 ectromelia	Q57316
33	171	5.5	18.2	320	Q57317	Q57317 ectromelia	Q57317
34	171	5.5	18.2	320	Q57318	Q57318 ectromelia	Q57318
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36	171	5.5	18.2	320	Q57320	Q57320 ectromelia	Q57320
37	171	5.5	18.2	320	Q57321	Q57321 ectromelia	Q57321
38	171	5.5	18.2	320	Q57322	Q57322 ectromelia	Q57322
39	171	5.5	18.2	320	Q57323	Q57323 ectromelia	Q57323
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52	171	5.5	18.2	320	Q57336	Q57336 ectromelia	Q57336
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54	171	5.5	18.2	320	Q57338	Q57338 ectromelia	Q57338
55	171	5.5	18.2	320	Q57339	Q57339 ectromelia	Q57339
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58	171	5.5	18.2	320	Q57342	Q57342 ectromelia	Q57342
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60	171	5.5	18.2	320	Q57344	Q57344 ectromelia	Q57344
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66	171	5.5	18.2	320	Q57350	Q57350 ectromelia	Q57350
67	171	5.5	18.2	320	Q57351	Q57351 ectromelia	Q57351
68	171	5.5	18.2	320	Q57352	Q57352 ectromelia	Q57352
69	171	5.5	18.2	320	Q57353	Q57353 ectromelia	Q57353
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72	171	5.5	18.2	320	Q57356	Q57356 ectromelia	Q57356
73	171	5.5	18.2	320	Q57357	Q57357 ectromelia	Q57357
74	171	5.5	18.2	320	Q57358	Q57358 ectromelia	Q57358
75	171	5.5	18.2	320	Q57359	Q57359 ectromelia	Q57359
76	171	5.5	18.2	320	Q57360	Q57360 ectromelia	Q57360
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83	171	5.5	18.2	320	Q57367	Q57367 ectromelia	Q57367
84	171	5.5	18.2	320	Q57368	Q57368 ectromelia	Q57368
85	171	5.5	18.2	320	Q57369	Q57369 ectromelia	Q57369
86	171	5.5	18.2	320	Q57370	Q57370 ectromelia	Q57370
87	171	5.5	18.2	320	Q57371	Q57371 ectromelia	Q57371
88	171	5.5	18.2	320	Q57372	Q57372 ectromelia	Q57372
89	171	5.5	18.2	320	Q57373	Q57373 ectromelia	Q57373
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98	171	5.5	18.2	320	Q57382	Q57382 ectromelia	Q57382
99	171	5.5	18.2	320	Q57383	Q57383 ectromelia	Q57383
100	171	5.5	18.2	320	Q57384	Q57384 ectromelia	Q57384
101	171	5.5	18.2	320	Q57385	Q57385 ectromelia	Q57385
102	171	5.5	18.2	320	Q57386	Q57386 ectromelia	Q57386
103	171	5.5	18.2	320	Q57387	Q57387 ectromelia	Q57387
104	171	5.5	18.2	320	Q57388	Q57388 ectromelia	Q57388
105	171	5.5	18.2	320	Q57389	Q57389 ectromelia	Q57389
106	171	5.5	18.2	320	Q57390	Q57390 ectromelia	Q57390
107	171	5.5	18.2	320	Q57391	Q57391 ectromelia	Q57391
108	171	5.5	18.2	320	Q57392	Q57392 ectromelia	Q57392
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111	171	5.5	18.2	320	Q57395	Q57395 ectromelia	Q57395
112	171	5.5	18.2	320	Q57396	Q57396 ectromelia	Q57396
113	171	5.5	18.2	320	Q57397	Q57397 ectromelia	Q57397
114	171	5.5	18.2	320	Q57398	Q57398 ectromelia	Q57398
115	171	5.5	18.2	320	Q57399	Q57399 ectromelia	Q57399
116	171	5.5	18.2	320	Q57400	Q57400 ectromelia	Q57400
117	171	5.5	18.2	320	Q57401	Q57401 ectromelia	Q57401
118	171	5.5	18.2	320	Q57402	Q57402 ectromelia	Q57402
119	171	5.5	18.2	320	Q57403	Q57403 ectromelia	Q57403
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122	171	5.5	18.2	320	Q57406	Q57406 ectromelia	Q57406
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125	171	5.5	18.2	320	Q57409	Q57409 ectromelia	Q57409
126	171	5.5	18.2	320	Q57410	Q57410 ectromelia	Q57410
127	171	5.5	18.2	320	Q57411	Q57411 ectromelia	Q57411
128	171	5.5	18.2	320	Q57412	Q57412 ectromelia	Q57412
129	171	5.5	18.2	320	Q57413	Q57413 ectromelia	Q57413
130	171	5.5	18.2	320	Q57414	Q57414 ectromelia	Q57414
131							

QY	4	CPOQKYIHPQNSICCTKCHKGTYLYNDCEGPNGLDTCRECNGIFTASENHLRHLSCS	63
Db	44	CPOQKYIHPQNSICCTKCHKGTYLYNDCEGPNGLDTCRECNGIFTASENHLRHLSCS	103
Qy	64	KCRKEMQVEISCTVDRDTCGCRKQHYWHSNLPFCFNCNLCLNGTIVHQISCKETON	123
Db	104	KCRKEMQVEISCTVDRDTCGCRKQHYWHSNLPFCFNCNLCLNGTIVHQISCKETON	163
RESULT	2		
ID	097530	PRELIMINARY;	PRT; 189 AA.
AC	097530;		
DT	01-MAY-1999	(TREMBrel. 10, Created)	
DT	01-MAY-1999	(TREMBrel. 10, Last sequence update)	
DT	01-JUN-2002	(TREMBrel. 21, Last annotation update)	
DE	Tumor necrosis factor receptor p60 (Fragment).		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butchera; Carnivora; Fissipedia; Felidae; Felis.		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
NCBI_TaxID	9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	MEDLINE:21109092; PubMed=11182158;		
RA	Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S., Bennett D.;		
RA	"Cloning of canine IL-1 α , TNFR and TNF-2,"; Vet. Immunol. Immunopathol. 78:207-214(2001).		
RL	EMBL; AFO13955; AAO01516_1; -.		
DR	HSSP; P19438; 1TNR.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR001361; TNFR_c6.		
DR	Pfam; PF00020; TNFR_c6; 3.		
DR	SMART; SM00208; TNFR_c6; 3.		
DR	PROSITE; PS01186; EGFR_2; UNKNOWN_1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.		
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.		
KW	Receptor.		
FT	NON_TER 189	189	
FT	SEQUENCE 189 AA; 21420 MW; F3FB0CE809D/D8E CRC64;		
Query Match	77.7%	Score 731;	DB 6;
Best Local Similarity	85.5%	Pred. No. 1.8e-73;	Length 189;
Matches	124;	Conservative 8;	Mismatches 13;
Indels	0;	Gaps 0,	
QY	4	CPOQKYIHPQNSICCTKCHKGTYLYNDCEGPNGLDTCRECNGIFTASENHLRHLSCS	63
Db	44	CPOQKYIHPQNSICCTKCHKGTYLYNDCEGPNGLDTCRECNGIFTASENHLRHLSCS	103
Qy	64	KCRKEMQVEISCTVDRDTCGCRKQHYWHSNLPFCFNCNLCLNGTIVHQISCKETON	123
Db	104	KCRKEMQVEISCTVDRDTCGCRKQHYWHSNLPFCFNCNLCLNGTIVHQISCKETON	163
QY	124	TWCTCHAGFPFLRENCVCSNCKS	148
Db	164	TWCTCHAGFPFLRENCVCSNCKK	188
RESULT	4		
ID	Q99MM1	PRELIMINARY;	PRT; 413 AA.
AC	Q99MM1;		
DT	01-JUN-2001	(TREMBrel. 17, Created)	
DT	01-JUN-2001	(TREMBrel. 17, Last sequence update)	
DT	01-JUN-2002	(TREMBrel. 21, Last annotation update)	
DE	WSL-1-like protein.		
GN	TNFRSF12.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
NCBI_TaxID	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=d129/SV;		
RX	MEDLINE:2118384; PubMed=11261933;		
RA	Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N., Owen M.J.;		
RT	"Genomic structure, expression, and chromosome mapping of the mouse homologue for the WSL-1 (Dr3, Apo3, TRAMP, LARD, Tr3, TNFRSF12) gene.," Immunogenetics 53:59-63 (2001).		
RT	Immunogenetics 53:59-63 (2001).		
DR	EMBL; AF329969; AAK12256_1; -.		
DR	HSSP; P25942; 1CDP		
DR	MGI; MGI:1934667; Tnfrsf12.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR001368; TNFR_c6.		
DR	Pfam; PF00531; death; 1.		
DR	SMART; SM0005; DEATH; 1.		
DR	SMART; SM00208; TNFR_c6; 3.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
OS	Felis silvestris catus (Cat).		
RESULT	3		
ID	Q95185	PRELIMINARY;	PRT; 189 AA.
AC	Q95185;		
DT	01-FEB-1997	(TREMBrel. 02, Created)	
DT	01-JUN-1998	(TREMBrel. 06, Last sequence update)	
DT	01-JUN-2002	(TREMBrel. 21, Last annotation update)	
DE	Tumour necrosis factor receptor p60 (Fragment).		
GN	TNFR-1		
OS	Felis silvestris catus (Cat).		

DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGR_1; UNKNOWN_1.
 DR PROSITE; PS0050; TNFR_NGR_2; 1.
 SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABBF CRC64;

RESULT 6
 ID Q91ZM6 PRELIMINARY;
 AC Q91ZM6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Tumor necrosis factor receptor type II (Fragment).
 OS Rattus norvegicus (Rtc).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAGUE-DAWLEY;
 RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
 RT "TNF-receptors P60 and P80 are constitutively expressed by rat brain capillary endothelial cells and participate in TNF-alpha transport through the blood-brain barrier.";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF420214; AAL1:021_1.
 DR InterPro; IPR01368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6.
 DR PROSITE; PS00652; TNFR_NGR_1; UNKNOWN_2.
 DR PROSITE; PS0050; TNFR_NGR_2; 3.
 KW Receptor.

Query Match Score 202; DB 11; Length 413;
 Best Local Similarity 31.4%; Pred. No. 2.3e-14;
 Matches 48; Conservative 19; Mismatches 58; Indels 28; Gaps 7;

Qy 18 CCTCKRGTYLYNDCPGPQDTDCCECSFTASENHLR-HCUCSKSKRKENGQVEISSL 76
 Db 54 CCRCGPKGHMNMKAPCAEPCGNSTCPCSDTFLTRDNHFKTDCTRQVCDEEALQVTLEN 11.3
 Qy 77 CTVDRTVCGCRKNQYRHYNSENLQCFNSCLCLNG-TYHSLC-----QBKNTVCT 127
 Db 114 CSAKSDTHCGQSG-----W-----CVDESTVPCKSSPFSCVPCGATTPVHEAPTBRP 162

Qy 128 CHAGFFLRENNEBCVSC-----SNCKKSLSBLCTKLIC 155
 Db 163 CLPGFYTRGNDCTSCTPTGFSSVCVKPA--CTAVC 193

RESULT 5
 ID Q9PVDA PRELIMINARY; PRT; 387 AA.
 AC Q9PVDA;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 OS DB-like transmembrane protein fullback.
 OC Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopidae; Xenopusspp.; Xenopus.
 OC NCBI_TaxID=83555;
 RN [1]
 RP SEQUENCE FROM N.A. Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
 RA "Identification and Characterization of fullback, a Novel Posteriorly-Expressed Xenopus Gene.";
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF11890; AAD54072.1; -.
 DR HSSP; P07174; INGR.
 DR InterPro; IPR001083; Copper-fist.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR01368; TNFR_C6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_C6.
 DR SMART; SM000015; DEATH; 1.
 DR SMART; SM000208; TNFR; 4.
 DR PROSITE; PS00017; DEATH DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGR_1; UNKNOWN_3.
 DR PROSITE; PS0050; TNFR_NGR_2; 4.
 KW Transmembrane.
 SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

RESULT 7
 ID Q9PUS0 PRELIMINARY;
 AC Q9PUS0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Decoy TNF receptor.
 OS Salvelinus fontinalis (Brook trout).
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Protactanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OC NCBI_TaxID=8038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2011001; PubMed=10642582;
 RA Bobe J., Goetz P.W.;
 RT "A tumor necrosis factor decoy receptor homologue is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
 RL Biol. Reprod. 62:420-426 (2000).
 DR HSSP; AF116738; AAC56428.1; -.
 DR InterPro; IPR00561; 1D4V.
 DR InterPro; IPR001368; TNFR_C6.

Query Match Score 193; DB 13; Length 387;
 Best Local Similarity 31.9%; Pred. No. 2.2e-13;
 Matches 53; Conservative 24; Mismatches 71; Indels 18; Gaps 10;

Qy 1 DSVCQPGKYTHPQNSICCTCKHGTLYNDCPGPQDTDCREC-EGSFTASENHLRHC 59
 Db 22 EDVCEGILY--TNSGKCCSCLCPAGFGVVPQ--GDSDTKCECIECNSTFDVRSAKC 76

Qy 60 LSCKSKRKEMGQVISSCTVDRDTVCGCRKNQYRHYNSENHLFCFNCSLCLNG-TYHSLC 11.8
 Db 77 QPCFTCQSPSLTLE-SNCRTQDVTCRERQLD--SNGI--CLPCOLCSKGHGTVSQ 13.1

Qy 119 QEKNTVCT-CHAGFFLRENNEBCVSCENCKSLSBLCTKLICLPQ 158
 Db 132 THKNTVQCQLSSGTYSEVKSSBSPCLPRTKEKETEVQIGDCVQP 177

Pfam:	PF00020;	TNFR_c6;	4.
DR	SMART;	SM00208;	TNFR_4.
DR	PROSITE;	PS01166;	EGF_2;
DR	PROSITE;	PS00652;	TNFR_NGFR_1;
DR	PROSITE;	PS50050;	TNFR_NGFR_2;
KW	Receptor;	302 AA;	34037 MW; B44C73477F05C3DF CRC64;
SQ	SEQUENCE:		
Query Match	20.0%;	Score 188;	DB 13;
Best Local Similarity	31.5%;	Pred. No. 6.1e-13;	Length 302;
Matches	45;	Conservative	21;
	Mismatches	53;	Indels 24;
	Gaps	7;	
QY	16	SICCTKHKGTLYNDCPGPGDTCRECEGSFTASENHLRHCUSKORKEMQVEIS	75
Db	33	SIVCDRDPPTGYLRAFCSAM-RKSDAECPKAGAYEFWNHISKCIRCSMCAE-NQVHQ	89
QY	76	SCTVDRITVCCRKNQYRHVYSENLFQCFNCSLC-----LNGTWHLSQEKONTVCT-	127
Db	90	ECSPSNICECEKREG--YVYNKKYFACIKHKECPGPGYANTGPH-----QPTECWQ	140
RESULT 8			
QDGH7	PRELIMINARY;	PRT;	285 AA.
AC	QDGH7;		
DT	01-MAR-2001 (TREMBlrel. 16, Created)		
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)		
DE	Fas ligand receptor soluble form (Fragment).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Osteiophysi; Cypriniformes;		
OC	Archosauria; Aves; Neognathae; Chordata; Vertebrata; Euteleostomi;		
OC	Gallus.		
RN	NCBI_TAXID=9031;		
RP	SEQUENCE FROM N.A.		
[1]	"		
RA	Bridgman J.T., Johnson A.L.: "Fas Expression and Regulation in Hen Granulosa Cells.";		
RA	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
RT	EML1; AF296875; AAC02243.1; -.		
DR	HSSP; Q14763; IDAV.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR001368; TNFR_c6.		
PFam	Pfam; PF00531; death; 1.		
DR	SMART; SM00208; TNFR_1.		
DR	PROSITE; PS00652; TNFR_NGFR_1;		
DR	PROSITE; PS50050; TNFR_NGFR_2.		
KW	Receptor.		
SQ	SEQUENCE:		
Query Match	19.1%;	Score 179.5;	DB 13;
Best Local Similarity	28.9%;	Pred. No. 6.3e-12;	Length 357;
Matches	45;	Conservative	15;
	Mismatches	53;	Indels 43;
	Gaps	3;	
QY	1	DSVCPOGS-KYTHPNNNICCTKHKGTLYNDCPGPGDTCRECEGSFTASENHLRHC	59
Db	38	DVSVCRLGEYPH---ENIICLNPAGTYKKAACAAEKGVCAPCEFFDTIEHDGLIKC	94
QY	60	LSCSKRKEMQVEISCTVDRITVCCRKNQYRHVYSENLFQCFNSCLNGTVHLSQ	119
Db	95	ISCDKCR--IDOBTTIEKCTSTONTRCKCR-----NGSFCL-----	127
QY	120	EKQNTVCTCHAGFLRNECVSGSNGERSLETKLC	155
Db	128	--PDQAC-----EVKKCSRCKEDEEERKSC	151
RESULT 10			
QDGH7	PRELIMINARY;	PRT;	320 AA.
AC	QDGH7;		
DT	01-JUN-1998 (TREMBlrel. 06, Created)		
DT	01-JUN-1998 (TREMBlrel. 06, Last sequence update)		
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)		
DE	Tumor necrosis factor receptor II homolog (V211).		
GN	CRMD.		
OS	Copox virus (CPV).		
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		
OC	Orthopoxvirinae.		
OX	NCBI_TAXID=10243;		
RN	SEQUENCE FROM N.A.		
RC	STRAIN:BRIGHTON;		
RX	MEDLINE=81188782; PubMed=9520445;		
RX	Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,		
RA	Bulter R.M.L., Pickup D.J., Esposito J.J.;		
RA	"A third distinct tumor necrosis factor receptor of orthopoxviruses."		
RT	Proc. Natl. Acad. Sci. U.S.A. 95:3786-3791(1998).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=BRIGHTON RED;		
RX	MEDLINE=83117629; PubMed=6961398;		

RA	Pickup D.J., Bastia D., Stone H.O., Joklik W.K.; "Sequence of terminal regions of cowpox virus DNA: arrangement of repeated and unique sequence elements.";	DE Murine tumour necrosis factor receptor 2 protein (Fragment).
RT		GN TNFRSF1B.
RT		OS Mus musculus (Mouse).
RL		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [3]
RN		NCBI_TaxID=10090;
RP	SEQUENCE FROM N.A.	RN [1]
RC	STRAIN=BRIGHTON RED;	RN SEQUENCE FROM N.A.
RA	Parsons B.L., Pickup D.J.; RT "Transcription of orthopoxvirus telomeres at late times during infection.";	RP STRAIN=NOD;
RT	RNA virology 175:69-80(1990).	RC RA
RN		RT Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.; RT "Amino acid variation in the tumor Necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice.";
RN		RT Genomics 0:0-0(0).
RP	SEQUENCE FROM N.A.	RN [2]
RC	STRAIN=NOD;	RN SEQUENCE FROM N.A.
RX	MEDLINE=90177240; PubMed=2309453;	RC RX MEDLINE=95178848; PubMed=7873884;
RA	Hu F.Q., Pickup D.J.; RT "Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution.";	RA RA
RT	RNA virology 181:716-720(1991).	RT RT "Allelic variation of the type 2 tumor necrosis factor receptor gene.";
RN		RT Mamm. Genome 5:726-727(1994).
RP	SEQUENCE FROM N.A.	RL DR EMBL: X76401; CA53981.1; -.
RC	STRAIN=BRIGHTON RED;	DR HSSP; P19436; INCF.
RX	MEDLINE=91196263; PubMed=2014445;	DR MGDB; MG1:1314883; Trifirstlib.
RA	Hu F.Q., Pickup D.J.; RT "Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution.";	DR InterPro: IPR01368; TNFR_c6.
RT	RNA virology 181:716-720(1991).	DR Pfam; PF00202; TNFR_c6_4.
RN		DR SMART; SM00208; TNFR_f4.
RP	SEQUENCE FROM N.A.	DR PROSITE; PS00652; TNFR_NGFR_1; 2.
RC	STRAIN=BRIGHTON RED;	DR PROSITE; PSS0050; TNFR_NGFR_2; 3.
RA	Parsons B.L., Pickup D.J.; RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.	KW Receptor.
RT	RNA [7]	FT NON_TER 1 1
RN	RP SEQUENCE FROM N.A.	FT VARIANT 87 87 S -> T.
RP	RC STRAIN=BRIGHTON RED;	FT VARIANT 93 93 T -> I.
RA	Dietrich F.S., Ray C.A., Sharma A.D., Pickup D.J.; RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.	FT VARIANT 268 268 F -> I.
RT	EMBL: U87234; AA:BB9434:4.1; -.	FT VARIANT 345 345 S -> C.
RN	DR HSSP; O14763; ID:OG.	FT VARIANT 421 421 Y -> C.
RP	DR InterPro: IPR001368; TNFR_c6.	SQ SEQUENCE 459 AA; 48686 MW; 6C5D2CFC1C4622DF CRC64;
RA	PFam: PF00020; TNFR_c6_2.	Query Match 18.7%; Score 176; DB 11; Length 459;
RT	DR SMART; SM00208; TNFR_NGFR_1; 2.	Best Local Similarity 31.1%; Pred. No. 2e-11; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;
RN	DR PROSITE; PS00652; TNFR_NGFR_2; 2.	QY 4 CPQGYIHPONNSICCTKCHKGTYLYNDCPGPQDQTTDCRECESGSFTASENHLRHCLSC- 62
RP	DR RECEPTOR: PSS0050; TNFR_c6_2.	Db 25 CQISQBYDRAQMCCAKCPQQYVRFHC-NKTSQDTVCDAEASYTQVNQFRCLSCS 83
RA	DR SEQUENCE 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	QY 63 SKCRKEMQVEISSCTVDRDTVGCRKQNY --- RHYWSLENFQCFNCSUCLNG-TVHLS 117
RT	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	Db 84 SSSTD--QVETRACTKQONRVCAEFGRYCALKTH-SSSCRCQMRSLSCGPFGFVASS 139
RN	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	Qy 118 COEKONTVC-TCHAGFFLRENICVSGCSNCKSLECTKLCLP 157
RP	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	Db 140 RAPNGNVVLKACAPGTF--SDTTSSTDVCRPHRICSIAlAP 178
RA	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	RESULT 12 Q9DGH8 PRELIMINARY; PRT; 312 AA.
RT	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	AC Q9DGH8; 16, Created
RN	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
RP	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	DT 01-MAR-2001 (TREMBLrel. 19, Last annotation update)
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	DE Fas antigen (Fragment).
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	GN FAS
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	OS Gallus gallus (Chicken)*
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	OC Gallo. NCBI_TaxID=9031;
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	OX RN [1]
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	RP SEQUENCE FROM N.A.
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	RA Brigham J.T., Johnson A.L.;
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	RT "Fas Expression and Regulation in Hen Granulosa Cells.";
OC	DR SEQUENCES 320 AA; 35234 MW; AA0DF0CBC47F7AB6 CRC64;	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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